

The frequency of heterozygotes for the seven sequence variants ranged from 3-11% among the 36 individuals tested. Some of the sequence variances appear to occur more commonly in certain racial or ethnic groups. For example, heterozygotes for four sequence variances (at nucleotides 1059, 1428, 3324 and 3375) were detected solely or predominantly in North American Blacks, with heterozygote frequencies of 1/4 or 2/4. The nucleotide 2538 variance was detected solely in North American Whites (4/16) and results in an amino acid exchange (see below). The nucleotide 3397 sequence variance was detected solely in one Japanese individual (of four tested).

The nucleotide 2538 sequence variant results in an aspartic acid vs. glutamic acid substitution at amino acid 740 of the 1024 amino acid protein. This residue lies in the cytoplasmic loop of the α 1 subunit.

The α 1 subunit of Sodium Potassium ATPase maps to chromosome 1p13-p11

The gene for the α 1 subunit of sodium-potassium ATPase has been mapped to chromosome band 1p13-p11 by several techniques. Yang-Feng et al. (10) assigned the ATP1A1 gene to 1p21-cen by Southern analysis of DNA from panels of rodent/human somatic cell hybrid lines. This localization was confirmed and refined by Chehab et al., who showed that the gene for the ATP1A1 subunit is on 1p13-p11 using hybridization to flow-sorted chromosomes and *in situ* hybridization (9).

Chromosome band 1p13-p11 is a site of frequent loss of heterozygosity

The short arm of chromosome 1 is comparatively well investigated for allele loss, especially in breast and colon cancers, however most of these studies are principally concerned with the 1p36 region, and there is comparatively little data on 1p13-p11. The best studies of proximal 1p allele loss are in breast and testicular cancers. These studies show LOH occurs in approximately 15-35% of breast cancers (11,12) and 15-25% of testicular cancers (13). Data from more distal loci on 1p show >25% LOH in

glioma, colon cancer, stomach cancer, ovarian cancer, and liver cancer (14). The LOH observed in this region indicates that other essential genes mapping to the 1p chromosomal arm, and especially to the 1p11 region, which have LOH and for which sequence variances, and therefore heterozygotes for a sequence variance, exist in normal somatic cells of individuals in a population are potential target genes

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Example 12: Ribonucleotide Reductase, M1 subunit (RRM1) - Target Gene VARIA200

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Ribonucleotide Reductase is essential for cell growth

Human ribonucleotide reductase (also called ribonucleoside diphosphate reductase) is essential in dividing cells for the production of deoxyribonucleotides prior to DNA synthesis in S phase. Ribonucleotide reductase catalyzes the reduction of all four

ribonucleoside diphosphates to the corresponding deoxyribonucleoside diphosphates by replacing the 2' hydroxyl moiety of ribose with a hydride ion to form deoxyribose; these reactions constitute the first committed steps in the creation of DNA precursors (deoxyribonucleotides), and are therefore tightly regulated by allosteric nucleotide binding sites on the M1 subunit (2,3). The enzyme is an $\alpha_2\beta_2$ tetramer apparently conserved in all prokaryotes and eukaryotes (1). The two subunits, M1 and M2, are both required for enzyme activity. The RRM2 subunit contains the catalytic site, while the RRM1 subunit provides an indispensable allosteric function. (See pages 758-763 of Biochemistry by C.K. Mathews and K.E. van Holde, Benjamin/Cummings Publishing Biochemistry, Company, Redwood City, 1990 for a fuller account of ribonucleotide reductase function.)

Both ribonucleotide reductase subunits are expressed in all proliferating cells but are generally nondetectable in quiescent cells. Ribonucleotide reductase subunit M2 is the target of several antineoplastic compounds, including hydroxyurea. Hydroxyurea is used in the chemotherapy of a variety of myeloproliferative disorders (4). It acts by reversibly destroying a tyrosyl free radical in the catalytic site of the M2 subunit (3). Hydroxyurea and other ribonucleotide reductase poisons are specific for the S phase of the cell cycle, resulting in growth arrest at the G1-S boundary and apoptotic death in tumor cells (5). Exposure of cell cultures to hydroxyurea results in selection of cells expressing high levels ribonucleotide reductase, demonstrating that ribonucleotide reductase is required for these cells to grow (6).

The human ribonucleotide reductase gene has sequence variances

The cDNA sequence of the human ribonucleotide reductase M1 subunit has been published by two groups (7,8). We undertook a systematic search for DNA sequence variance in the cDNA of the M1 subunit by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed using

the sequence of Parker et al. (GENBANK accession X59543; see ref. 7). SSCP analysis revealed 4 sequence variances, and subsequent DNA sequence analysis confirmed that nucleotides 1037 (C vs. A), 2410 (A vs. G), 2419 (A vs. G) and 2717 (T vs. A) vary as shown in the Target Summary Table. (The sequence variance at nt 1037 was previously noted by Parker et al., ref. 7.) Also, DNA sequencing revealed an insertion/deletion sequence variance: the 9 consecutive T nucleotides between positions 2724 and 2732 (numbering from ref. 7) were augmented in some cDNAs by a tenth T. (This sequence variance is designated T9 vs. T10 in the Target Summary Table.)

Both alleles at nt 1037 were detected in North American Whites, Hispanics, Chinese, Japanese, Arabs and Indians. Similarly, both alleles of the sequence variance at nt 2410 were detected in virtually all tested populations: North American White, North American Black, Hispanic, Chinese, Arab and Indian. In contrast, the sequence variances at nt 2419 and 2717 were prevalent in North American Blacks, Hispanics, Chinese, and Japanese, but not North American Whites. The insertion/deletion sequence variance at nt 2724 was only studied in four individuals so no firm conclusions can be drawn regarding population distribution, however it appears to be in linkage disequilibrium with the 2419 and 2724 sequence variances.

The human ribonucleotide reductase gene maps to chromosome 11p15.5

The gene for human ribonucleotide reductase has been mapped to band 11p15.5 by several techniques. Initially the gene was localized by Southern hybridization analysis of human X rodent somatic cell hybrids and by chromosomal *in situ* hybridization (9). Subsequently RRM1 has been placed on a yeast artificial chromosome (YAC) physical map of chromosome 11p15 (10). The precise physical localization of the RRM1 gene facilitates interpretation of LOH results at adjacent polymorphic markers (see below).

Chromosome band 11p15.5 is a site of frequent loss of heterozygosity

The short arm of chromosome 11 is the site of several tumor suppressor genes, including the WT1 gene and the Beckwith-Weidemann syndrome gene. As a result there are many studies of LOH in 11p15.5, particularly focusing on breast, cervix, kidney, liver, lung, ovarian, stomach and testicular cancers. These studies show that the 11p15.5 band of chromosome 11 is frequently reduced to one copy (11-28). For example, LOH occurs in approximately 13-33% of breast cancers (11-13), 14-42% of cervical cancers (14), 0-50% of liver cancers (16), 0-80% of lung cancers (17-19), 18-54% of ovarian cancers (20,21), 0-71% of stomach cancers (22) and 0-50% of testicular cancers (23,24). Other studies show that 11p15.5 LOH may also be frequent in bladder cancer (25), esophageal cancer (26), some leukemias (27) and sarcomas (28). Many deletions in the 11p15.5 region span relatively short chromosomal segments (2 - 10 megabases; see ref. 17).

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Example 13: Thymidylate Synthase (TS) - Target Gene VARIA250*Thymidylate Synthase is essential for cell growth*

5 Human thymidylate synthase (TS) catalyzes the formation of thymidine monophosphate (dTMP) from deoxyuridine monophosphate (dUMP) by transfer of a methyl group from N5,N10-methylenetetrahydrofolate to carbon 5 of dUMP. This is the sole *de novo* pathway to dTMP, an essential precursor for DNA synthesis. TS also plays an important role in balancing the four nucleotide precursors for DNA polymer synthesis (1). Thus TS is an attractive target for antiproliferative drugs. (See Biochemistry by C.K. Mathews and K.E. van Holde, Benjamin/Cummings Publishing Company, Redwood City, 1990, pages 763-768, for a fuller account of thymidylate synthase function.)

15 Like some other growth associated genes involved in DNA synthesis, thymidylate synthase is expressed in proliferating cells at 20-40 fold higher levels than in quiescent cells. Increased expression occurs at the G1-S transition of the cell cycle when quiescent cells are stimulated with serum. Levels of thymidylate synthase are finely controlled by autoregulatory feedback loops wherein TS protein regulates the transcription, stability and translational efficiency of TS mRNA (2). Transcription increases by only 2-4 fold, so posttranscriptional events constitute the predominant regulatory mechanisms (3). One mechanism of 5-FU resistance is increased expression of TS Mrna.

25 Thymidylate synthase is the target of 5-fluorouracil (5-FU), a potent antineoplastic compound. Once inside cells 5-FU is ribosylated and phosphorylated to 5-fluoro-2'-deoxyuridine 5'-monophosphate (F-dUMP), which acts as an inhibitory transition state analog of TS when bound in the presence of the enzyme's second substrate, N5,N10-methylenetetrahydrofolate. (5-FU is also incorporated into both DNA and RNA,

augmenting its toxicity.) 5-FU induces partial responses in 10-30% of patients with a variety of cancers, including metastatic breast and gastrointestinal tract cancers (4). While 5-FU is a potent antiproliferative agent in tissue culture cells, as with most antineoplastic drugs, its clinical utility is limited by lack of discrimination between normal cells and tumor cells: common toxic effects include stomatitis, diarrhea, bone marrow suppression, hair loss and occasionally cardiac and neurologic symptoms.

The human thymidylate synthase gene has sequence variances

The sequence of a human thymidylate synthase cDNA was determined by Takeishi et al. (5), who later determined the genomic sequence as well (6). We undertook a systematic search for DNA sequence variance by analysing 36 unrelated individuals using the single strand conformation polymorphism. Primers were designed using the sequence of Takeishi et al. (5). SSCP analysis revealed 3 DNA fragments having sequence variances, and subsequent DNA sequence analysis showed that nucleotides 1066 (C vs. T), 1136 (A vs. G) and 1497 (A vs. T) vary among normal individuals as shown in the Target Summary Table. All three sequence variances are in the 3' untranslated region of the gene. The nucleotide 1066 and 1497 sequence variances are in complete linkage disequilibrium in the 36 individuals examined. Both alleles of all three sequence variances were detected in North American Whites, North American Blacks, Chinese, Japanese, Arabs and Indians.

Another TS sequence variance has been described by Berger and colleagues (7-9). They detected a T to C change at nucleotide 276 of the TS gene, resulting in the substitution of histidine for an evolutionarily conserved tyrosine at residue 33 of TS protein. So far the histidine allele has been detected in only one cell line, HCT116 (7). The rare his-33 form of the protein is 3-4 fold more resistant to FdUrd than the tyr-33 form, due to an 8 fold lower catalytic efficiency (kcat), suggesting that histidine at residue 33 perturbs the structure of the TS active site (9)

The human thymidylate synthase gene maps to chromosome 18p11.32

5 The gene for human thymidylate synthase was initially mapped to the long arm of chromosome 18 (18q21.31-qter) by somatic cell hybrid analysis (10), however two subsequent reports place the gene in band 18p11.32 using fluorescence *in situ* hybridization (11,12).

Chromosome band 18p11.32 is a site of loss of heterozygosity

10 The long arm of chromosome 18 contains the DCC (deleted in colon cancer) candidate tumor suppressor gene and has been well studied in a variety of tumors. The short arm (18p), where TS apparently resides, has not been studied as extensively. The available data suggests there is LOH in approximately 45% of colon cancers (13) and 25-30% of cervical (14), head and neck (15), lung (16) and ovarian (17) cancers and sarcomas.

15 LOH has also been described in breast, brain, esophagus, kidney and prostate cancers (0-15%). 18p has not been studied for allele loss in several other major cancers, including bladder, leukemia, lymphoma, liver, pancreas, stomach and testicular cancers.

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Example 14: Cytidine Triphosphate Synthetase (CTPS) - Target Gene VARIA260

Cytidine Triphosphate Synthetase is essential for cell growth

Human cytidine triphosphate synthetase catalyzes the glutamination of UTP to form CTP. The reaction is: $UTP + ATP + \text{glutamine} \rightarrow CTP + ADP + P_i + \text{glutamate}$. This is the rate limiting step in the synthesis of cytidine nucleotides from both the *de novo* and uridine salvage synthesis routes (see ref. 1 and references therein). CTPS also plays a vital regulatory function in balancing nucleotide pools for DNA polymer synthesis; it is allosterically regulated by CTP (negatively) and GTP (positively).

There is compelling evidence that CTPS is essential for cell survival:

CTPS is evolutionarily conserved in yeast and bacteria, with a high degree of amino acid identity in regions mediating allosteric regulation and catalysis (1-

3). (Another example: the human and hamster enzymes are identical in length and 98% amino acid identical over 591 amino acids.)

Mutant hamster cells lacking functional CTPS need exogenous cytidine to survive (3).

5 There is no known human deficiency disease of CTPS.

CTPS function is increased in proliferating cells (4).

10 Thus CTPS is an attractive target for antiproliferative drugs. Cyclopentyl cytosine (CPE-C) is a synthetic cytidine analog in which a cyclopentyl group replaces the furan ring of the ribose sugar. CPE-C has antineoplastic and antiviral effects in animal models (5). The drug is kinased intracellularly to the triphosphorylated nucleotide form (CPE-CTP). Exposure of cells to CPE-C leads to rapid depletion of CTP pools, as a result of inhibition of CTPS by CPE-CTP (6,7). Upregulation of CTP synthetase, or loss of negative allosteric modulation by CTP is associated with resistance to the cancer chemotherapy drugs arabinosyl cytosine (ara-C), 5-fluorouracil and other
15 cytotoxic nucleoside analogs as well as alkylating agents (3).

The human cytidine triphosphate synthetase gene has sequence variances

20 The sequence of a human cytidine triphosphate synthetase cDNA was determined by Yamauchi et al. (1), who later determined the genomic sequence as well (2). We undertook a systematic search for DNA sequence variance by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed using the sequence of Yamauchi et al. (1). SSCP analysis revealed 3
25 DNA fragments having sequence variances, and subsequent DNA sequence analysis showed that nucleotides 576 (A vs. G), 2093 (C vs. T) and 2135 (G vs. A) vary among normal individuals as shown in the Target Summary Table. The nucleotide 576 sequence variance is a silent substitution in the coding region, while the latter two sequence variances are in the 3' untranslated region of the cDNA. All three sequence

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variances were detected at low frequency in the panel of 36 individuals (3-8%), however all but one of the heterozygotes is Asian, and it seems likely that a larger survey of Asian populations would show higher allele frequencies in Chinese and other groups. For example among the four Chinese in the panel two (50%) are heterozygous for the residue 2135 sequence variance, and one (25%) is heterozygous for the nt 576 sequence variance. Also, the one Cambodian in the panel is heterozygous for both the 2093 and 2135 sequence variances.

The human cytidine triphosphate synthetase gene maps to chromosome 1p34.1

The gene for human cytidine triphosphate synthetase has been mapped to 1p34.1 by somatic cell hybrid analysis (2).

Chromosome band 1p34.1 is a site of frequent loss of heterozygosity

The short arm of chromosome 1 is comparatively well investigated for allele loss, especially in breast and colon cancers. The 1p35-32 and 1p22-13 regions flank 1p34.1 and are the best available markers for LOH on 1p. Studies of these regions show 30-50% LOH frequency in breast cancer (8-12), 41-75% in glioma (a brain cancer subtype) (13), 20-40% in colon cancer (14,15), ~50% in stomach cancer (16), ~20% in lung cancer (17) and 20-30% in ovarian cancer (18). High frequency LOH has been detected in several uncommon cancers such as pheochromocytoma (50-86%) and neuroblastoma (~50%). Most other common cancers have not been adequately investigated to assess LOH frequency in this region.

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Example 15: Cysteinyl tRNA Synthetase (CARS) - Target Gene VARIA301

The human cysteinyl tRNA synthetase gene is essential for cell survival

Cysteinyl-tRNA synthetase (CARS) catalyzes ATP dependent covalent attachment of

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cysteine to its cognate tRNA to form cysteinyl-tRNA. In the absence of cysteinyl-tRNA, protein synthesis is blocked. Since Cysteinyl-tRNA synthetase is a single copy gene in man, inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

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The human cysteinyl-tRNA synthetase gene and mRNA have sequence variances

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A human cDNA encoding cysteinyl tRNA synthetase (CARS) was cloned based on the similarity of a human expressed sequence tag (EST) to *E. coli* cysteinyl tRNA synthetase (1). The published human CARS cDNA is 2048 nucleotides in length and includes a 30 nucleotide 5' untranslated region followed by an open reading frame of 1914 nucleotides and a 3' untranslated region of 134 nucleotides (1). An EMBL/GENBANK submission (accession # L06845) by the authors of ref. 1 includes a 3' untranslated region 423 nucleotides longer than the published sequence, but lacks 19 consecutive A nucleotides after position 2029 (making a net increase of: $423 - 19 = 404$ nucleotides, and a composite cDNA of: $2048 + 404 = 2452$ nucleotides in length. We have confirmed the existence of 2452 nt transcripts by PCR amplification of reverse transcribed mRNA.) We designed primers as shown on the annotated cDNA sequence and screened the composite 2452 nt cDNA for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism (SSCP) technique. Two sequence variances were identified. One of the sequence variances, located in the 5' untranslated region, was below the desired level of 20% heterozygosity. The other sequence variance is a C vs. T transition near the 3' end of the coding sequence at nucleotide 1739 (see annotated sequence).

The human cysteinyl tRNA synthetase protein has sequence variances

The deduced amino acid sequence of the human CARS gene encodes a protein of 638 amino acids which probably functions as a monomer, by analogy to related synthetases. The deduced protein contains two sequence motifs, HIGH (residues 64-

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67) and KMSKS (residues 406-410), which define Class I synthetases (see ref. 2 for background information on tRNA synthetases). These two conserved motifs form an ATP binding fold (the Rossman fold) in the amino terminal half of the protein. Cytosine at nucleotide 1739 encodes proline at residue 622 of the protein, while
5 thymine at nucleotide 1739 encodes leucine. The pro/leu amino acid sequence variance is a mere 16 residues from the C terminus of the protein. The C-terminal portion of CARS, by analogy to other class I synthetases, contains the tRNA binding site.

10 *Frequency of CARS heterozygotes*

The frequency of heterozygotes for the nucleotide 1739 sequence variance is ~45-50% in all major racial groups surveyed (see accompanying table), including North American Whites (8/15=53%), North American Blacks (2/4=50%), Chinese
15 (2/4=50%), Swedish (127/344=37%) and Japanese (1/4=25%). The wide population distribution of both alleles suggests that other population groups will also have a high frequency of heterozygotes.

20 *Gene Mapping of CARS to 11p15.5*

Human CARS cDNA has been mapped to chromosome 11p15.5 by screening human X Chinese hamster somatic cell hybrids informative for all human chromosomes, and by fluorescence *in situ* hybridization (3). Both mapping techniques were conclusive in showing only one locus for human CARS. Detailed physical maps of 11p15.5 have
25 subsequently allowed precise localization of the CARS gene relative to other DNA markers (4).

LOH at 11p15.5 is well documented in many cancer types

The short arm of chromosome 11, and particularly the 11p15.5 region, is deleted in a

variety of human cancers, including (but not limited to) ovarian (18 - 50% LOH), non-small cell lung (22 - 71%), breast (12 - 33%), bladder (40 - 50%), esophageal (18 - 40%) and testicular cancers (18 - 66%) (refs. 5-12). Many deletions in the 11p15.5 region span relatively short chromosomal segments (2 - 10 megabases; see ref. 8).

5 Using the specific variances identified in the CARS gene as markers for heterozygosity, we have determined that LOH occurs in 10/20 ovarian cancers (50%) and 10/52 non-small cell lung cancers (19%).

Assays for human CARS inhibitors

10 There is no published work on the protein encoded by the putative human CARS cDNA, nor on any other eukaryotic CARS protein, however the extensive characterization of other Class I synthetases from both prokaryotes and eukaryotes provides a template for modeling the structure of human CARS. (For an example of
15 how this can be done see ref. 14, in which the three dimensional structure of human alanyl-tRNA synthetase has been modeled up to amino 249 by neural net software and multiple alignments of partial and complete human AARS sequences with heterologous prokaryotic class II synthetases for which crystal structures exist.) With
20 respect to the C-terminal location of the variant amino acid residue in human CARS, it is worth noting that single amino acid substitutions in the C-terminal region of alanyl tRNA synthetase can have greater than 100 fold effects on catalytic activity (15).

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Example 16: Glutamyl-Prolyl tRNA Synthetase (EPRS): - Target Gene VARIA300

The human glutamyl-prolyl tRNA synthetase gene is essential for cell survival

Glutamyl-prolyl-tRNA synthetase (EPRS) catalyzes ATP dependent covalent attachment of glutamine and proline to their cognate tRNAs to form glutamyl-tRNA and prolyl-tRNA. In the absence of glutamyl-tRNA or prolyl-tRNA, protein synthesis is blocked. Since glutamyl-prolyl-tRNA synthetase is a single copy gene in man, inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

The human glutamyl-prolyl tRNA synthetase gene, mRNA and protein have sequence variances

A human cDNA encoding glutamyl-prolyl tRNA synthetase (EPRS) was initially misidentified as glutaminyl-tRNA synthetase (1) based on misleading sequence alignments with bacterial and yeast glutaminyl-tRNA synthetase (2). Subsequently, biochemical studies of the protein encoded by a *D. melanogaster* gene ~70% identical to the human gene demonstrated glutamyl (not glutaminyl) tRNA synthetase activity, and also showed that a single gene encodes both glutamyl- and prolyl-tRNA synthetases in the fly (3). These observations eventually led to the realization that

human EPRS is also a single polypeptide containing two synthetases (2). The aminoacyl tRNA synthetases are divided into two classes (see *Background on tRNA Synthetases*, above). Glutamyl-tRNA synthetase belongs to Class I while Prolyl-tRNA synthetase belongs to class II. Thus the two halves of EPRS evolved independently and likely represent an evolutionarily recent fusion. The published human EPRS cDNA is 4,586 nt long and includes a 5' untranslated region of 58 nt followed by an open reading frame of 4320 nt and a 3' untranslated sequence of 208 nt (1). The gene encodes a polypeptide of 1440 amino acids. The glutamyl-tRNA synthetase activity is encoded by an imprecisely defined segment at 5' end of the gene probably spanning at least amino acids 105-426, while the prolyl-tRNA synthetase activity is encoded by a segment likely including residues 942-1369 at the 3' end of the gene (2). The two synthetase moieties are connected by a central domain of unknown function. It has been speculated that the central domain may attach the enzyme to the cytoskeleton or to other aminoacyl-tRNA synthetases in a multienzyme complex (2, 3).

The human glutamyl-prolyl-tRNA synthetase gene and mRNA have sequence variances

We designed primers and screened the 4586 nt cDNA for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism technique. Seven sequence variances were identified, four located in the coding sequence and three located in the 3' untranslated region. As shown on the Annotated Glutamyl-Prolyl tRNA Synthetase cDNA Sequence and in the Target Summary Page, the sequence variance nucleotides are 2520 (C vs. A), 2944 (G vs. A), 2963 (C vs. T), 2969 (A vs. G), 3247 (A vs. G), 4459 (G vs. A) and 4506 (G vs. A). The sequences flanking the alternate allelic forms and their frequencies of occurrence are shown on the Target Summary Page. Less than 10% of individuals surveyed are heterozygous for sequence variances at 2520, 2944 and 2963. Heterozygotes for the other 4 sequence variances occur more frequently and appear to be widely distributed in the surveyed populations (see below).

The human glutamyl-prolyl tRNA synthetase protein has sequence variances Three nucleotide sequence variances, at 2520, 2963 and 2969, alter the amino acid coding sequence of EPRS at residues 821 (pro/his), 969 (his/tyr) and 971 (ile/val). The residue 821 his and 969 tyr alleles are relatively rare, with fewer than 10% heterozygotes in the surveyed populations. The more common residue 971 sequence variance lies in the PRS domain of the protein, near one of the widely conserved defining motifs for class II tRNA synthetases.

EPRS heterozygotes are frequent in non-Asian populations. While the overall frequency of residue 971 heterozygotes is 8/36 (24%), the frequency of heterozygotes varies among different populations. For example, there are no heterozygotes among 10 Asians surveyed (Chinese, Japanese, Filipino and Korean), while 8/26 (31%) of non-Asians, including North American Whites, Blacks and Hispanics, are heterozygotes.

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The EPRS Gene Maps to 1q41-q42

Human EPRS cDNA has been mapped to chromosome 1q41-42 by screening human X Chinese hamster somatic cell hybrids informative for all human chromosomes, and by fluorescence *in situ* hybridization (3). Both mapping techniques were conclusive in showing only one locus for human EPRS.

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Loss of heterozygosity at 1q41-42 is documented in several cancer types. 17-25% of breast cancers have allele loss in the 1q41-q42 region (4, 5), 29-46% of colon cancers (6, 7) and 17-26% of cervical cancers (8). One report describes 27% LOH in stomach cancer (9). One or two studies of brain, esophageal, kidney, liver and ovarian cancers also report LOH. No studies of LOH in the 1q41-q42 region have been reported in bladder, endocrine, head and neck, lung, or pancreas cancers or in leukemia or lymphoma.

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Antisense considerations The sequence variances at 2963 and 2969 are close enough that a 20-mer antisense oligonucleotide could easily span them. Such an oligonucleotide should afford greater allele discrimination than is possible with a single nucleotide difference. However, the 2963 sequence variance is fairly rare (<10% heterozygotes) and not in linkage disequilibrium with the 2963 sequence variance, so there are more than two haplotypes in the populations tested.

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Example 17: Alanyl-tRNA Synthetase (AARS) - Target Gene VARIA304

The human glutamyl-prolyl tRNA synthetase gene is essential for cell survival

Alanyl-tRNA synthetase (AARS) catalyzes ATP dependent covalent attachment of alanine to its cognate tRNA to form alanyl-tRNA. In the absence of alanyl-tRNA, protein synthesis is blocked. Since alanyl-tRNA synthetase is a single copy gene in man (see below) inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

The human alanyl-tRNA synthetase gene and mRNA have sequence variances

A human cDNA encoding alanyl tRNA synthetase (AARS) was cloned by Shiba et al. (1) using cross species PCR: AARS sequences from four evolutionarily distant species were compared and primers were designed to conserved regions specific to AARS. The cloned human cDNA is 3344 nt in length and includes a 110 nt 5' untranslated region, an open reading frame of 2904 nt encoding a 968 residue polypeptide, and a 3' untranslated region of 330 nt (ref. 1; Genbank accession D32050).

We designed primers. The 3344 nt cDNA was screened for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism (SSCP) technique. One sequence variance was identified, a C vs. T transition at nucleotide 1013, within the coding sequence. The published nucleotide at position 1013 is T (1).

The frequency of AARS heterozygotes is 25-50% in all populations surveyed. The frequency of heterozygotes for the nucleotide 1013 sequence variance is 57% in the 36 individuals tested. Both alleles are present in all major racial groups surveyed (see Target Gene Summary Table), including North American Whites (9/15=60% heterozygotes), North American Blacks (3/4=75%), Chinese (2/4=50%), Japanese (1/4=25%) and Hispanic (1/2). The wide population distribution of both alleles suggests that other population groups will also have a high frequency of heterozygotes.

The AARS gene maps to 16q22

The human AARS cDNA has been mapped to chromosome 16q22 by us and by Nichols et al. (ref. 2). We designed primers to the 3' untranslated region of AARS and used PCR to analyze the National Institute of General Medical Sciences (NIGMS) Human/Rodent Somatic Cell Hybrid Mapping Panel #2 (see page 704 of the NIGMS 1994/1995 Catalog of Cell Lines, available from the Coriell Cell Repository, Camden, NJ). The panel consists of 24 hybrid cell lines, each monochromosomal for one human chromosome. The AARS PCR product mapped to the hybrid containing human chromosome 16. Subsequently we screened the Radiation Hybrid Mapping Panel created at Stanford University (rhserver@shgc.stanford.edu) and distributed by Research Genetics (RH01). The AARS PCR product mapped near D16S496 with a lod score >10. D16S496 is a polymorphic DNA marker at 16q22. The AARS PCR product mapped near D16S496 with a LOD score >10. DH16S496 is a polymorphic DNA marker at 16q22. (See, ref. 29 for a full explanation of modification hybrid mapping.) Similar results were obtained by Nichols et al., who mapped AARS by analysis of the same NIGMS hybrid mapping panel, by PCR mapping in a chromosome 16 regional mapping panel and by fluorescence *in situ* hybridization to metaphase chromosomes. All mapping techniques were conclusive in showing only one locus for human AARS.

LOH at 16q22 is well documented in many cancer types. Loss of heterozygosity studies of chromosome 16q have principally focused on breast and liver cancers. In six detailed studies of breast cancer in the 16q22 region LOH frequencies of 40-60% have been reported (refs 3-8). 16q22 LOH has been reported in 25-90% of liver cancers (9-13), with the average around 45%. Less extensive studies of other cancer types report 16q22 LOH in 19% of bladder cancers, 20% of colon cancers (14), 19-27% of esophageal cancers (15), 25% of small cell lung cancers (16), 16-37% of ovarian cancers (17-19) and 22% of uterine cancers (20), and 31-50% of prostate cancers (21-

22).

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Example 18: Threonyl-tRNA Synthetase (TARS) - Target Gene VARIA302

The human threonyl-tRNA synthetase gene is essential for cell survival

10 Threonyl-tRNA synthetase (TARS) catalyzes ATP dependent covalent attachment of
threonine to its cognate tRNA to form threonyl-tRNA. In the absence of threonyl-
tRNA, protein synthesis is blocked. Threonyl-tRNA synthetase is a single copy gene
in man (see below) and inhibition of TARS is cell lethal. This has been shown using
the specific TARS inhibitor borrelidin, a threonine analog. Borrelidin resistant CHO
15 cell lines have been isolated; the most resistant lines contain ~60-100 fold more
immunologically reactive protein and 10-20 fold higher TARS activity than non-
selected CHO cells (1-3).

20 The human TARS enzyme is a homodimeric member of the class II tRNA synthetases.
The human protein is 53% amino acid identical to *S. cerevisiae* cytoplasmic TARS,
40% amino acid identical to *E. coli* TARS and 39% amino acid identical to yeast
mitochondrial TARS. The degree of evolutionary conservation is 52-64% when
conservative substitutions are allowed.

25 *The human Threonyl-tRNA synthetase gene and mRNA have sequence variances.* A
human cDNA encoding threonyl tRNA synthetase was cloned by Cruzen and Arfin
(GENBANK accession M63180; ref. 2) using anti-TARS antibodies to screen a lgt11
expression library. The cDNA is 2644 nt in length and includes a 138 nt 5' untranslated
region, an open reading frame of 2136 nt encoding a 712 residue polypeptide, and a 3'

untranslated region of 370 nt.

We designed primers for amplification. The 2644 nt cDNA was screened for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism (SSCP) technique. Three sequence variances were identified: G vs. A transitions at nucleotides 1608 and 1755 within the coding sequence, and a C vs. T transition at nucleotide 2395 of the 3' untranslated region. None of the sequence variances alters the sense of the coding strand. The published sequence shows G, G and T at the three sequence variance sites

The frequency of TARS heterozygotes is 25-45% in all populations surveyed. The nucleotide 1608 sequence variance was genotyped only in North American Whites, 45% of whom were heterozygotes. The nucleotide 1608 and 1755 sequence variances were both genotyped in 36 individuals, with overall heterozygosity rates of 31% and 25%, respectively. Both sequence variances were detected in North American Whites, North American Blacks, Hispanics and Chinese. Of 14 North American Whites genotyped at all 3 sequence variance nucleotides, 11 (79%) were heterozygous for a least one polymorphism (see threonyl tRNA synthetase summary table).

The TARS gene maps to 5p13-CEN. The human TARS cDNA has been mapped to chromosome 5p13-CEN by analysis of TARS isoelectric focusing patterns in human/Chinese hamster hybrids (). The mapping studies were consistent with one human TARS locus.

LOH at 5p13-CEN is documented in several cancer types. The best data on 5p LOH is in cervical cancer where 9 markers have been tested in 3 different studies. The frequency of LOH ranges from 12-57%, averaging ~45%. Other cancers that have been studied are breast (10-24% LOH), head and neck (20% LOH), adenocarcinoma of the lung (40% LOH, but only 5 cancers were studied), melanoma (40%) and ovary (15-

21%).

Assays for human TARS inhibitors. Human TARS protein is a homodimeric class II synthetase. Antibodies to rat TARS were used to clone the human protein. The high degree of amino acid conservation throughout the protein suggests that it may be possible to create yeast and/or bacterial strains with human CARS.

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15 **Example 19: Glutaminyl-tRNA Synthetase (QARS) - Target Gene VARIA305**

The human glutaminyl-tRNA synthetase gene is essential for cell survival

20 Glutaminyl-tRNA synthetase (QARS) catalyzes ATP dependent covalent attachment of glutamine to its cognate tRNA to form glutaminyl-tRNA. In the absence of glutaminyl-tRNA, protein synthesis is blocked in eucaryotic cells. Glutaminyl-tRNA synthetase is a single copy gene in man. Inhibition of its function is expected to be cell lethal, as shown for other tRNA synthetases (summarized above).

25 *The human Glutaminyl-tRNA synthetase gene and mRNA have sequence variances.*

A human cDNA encoding glutaminyl tRNA synthetase (QARS) was cloned by Lamour et al. (1) who expressed the cDNA in *E. coli* and demonstrated glutaminyl tRNA synthetase activity in bacterial extracts. The cloned human cDNA

(Genbank/EMBL accession number X76013) is 2437 nt in length and includes a 5' untranslated region of 5 nucleotides, an open reading frame of 2325 nucleotides encoding a 775 amino acid polypeptide, and a 3' untranslated region of 107 nt including 8 terminal nt of poly A.

5

We designed primers for amplification. The QARS cDNA was screened for sequence variance in 36 unrelated individuals using the single strand conformation polymorphism (SSCP) technique. One sequence variance was identified, a C vs. T transition at nucleotide 404, within the coding sequence. The published nucleotide at position 404 is C. The sequence variance does not affect the protein encoded.

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The frequency of heterozygotes for the nucleotide 404 sequence variance is 11% in the 36 individuals tested (4/36). However three of 16 North American Whites are heterozygotes (19%), and one of four Japanese (25%) (see Target Gene Summary Table).

15

The QARS gene maps to 3p

The human QARS cDNA has been mapped to chromosome 3 by hybridization of a QARS probe to a panel of 25 human/rodent somatic cell hybrids (1). One somatic cell hybrid, not known to contain human chromosome 3, was positive for both the QARS probe and an ACY1 probe. ACY1 maps to human 3p21, suggesting QARS may also map in this area. We independently mapped QARS to chromosome 3 using primers from the 3' untranslated region to analyze the National Institute of General Medical Sciences (NIGMS) Human/Rodent Somatic Cell Hybrid Mapping Panel #2 by PCR (see page 704 of the NIGMS 1994/1995 Catalog of Cell Lines, available from the Coriell Cell Repository, Camden, NJ). The panel consists of 24 hybrid cell lines, each monochromosomal for one human chromosome. The QARS PCR product mapped to the hybrid containing human chromosome 3. All mapping techniques were conclusive

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in showing only one locus for human QARS.

Chromosome band 3p21 is a site of frequent loss of heterozygosity. The short arm of chromosome 3 has been well studied in breast, cervical, esophageal, kidney, and lung cancers. These studies report frequent allele loss at 3p21, varying up to 100% in some studies of small cell lung cancer. Among other cancers LOH occurs in approximately 20-30% of breast cancers (2,3), 30-60% of cervical cancers (4,5), 10-40% of esophageal cancers (6,7), 45-80% of kidney cancers (8-10), 50-100% of nasopharyngeal cancers (11), 0-75% of squamous cell head and neck cancers (12), 30-60% of melanomas (13), 30-100% of non-small cell lung cancers (14-16) and 80-100% in small cell lung cancer (17-19). Other for which there are reports of LOH in at least 20% of cases include leukemia, pancreas cancer, sarcoma, testis cancer and ovarian cancer. Other cancer types, including bladder and lymphoma, have not been studied for LOH at 3p21.

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Example 20: Lysyl-tRNA Synthetase (KARS) - Target Gene VARIA303

Human Lysyl t-RNA synthase gene is essential

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Lysyl-tRNA synthetase (KARS) catalyzes ATP dependent covalent attachment of lysine to its cognate tRNA to form lysyl-tRNA. In the absence of lysyl-tRNA, protein synthesis is blocked. Since lysyl-tRNA synthetase is a single copy gene in man, inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

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The human Lysyl-tRNA synthetase gene and mRNA have sequence variances

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A human cDNA encoding a sequence similar to bacterial lysyl tRNA synthetases was cloned by Nomura et al. (GenBank/DDBJ submission D31890; see ref. 1) while sequencing random cDNAs. No biochemical studies of the protein encoded by this sequence have been reported. The 5' end of the sequence apparently begins in the coding region and the open reading frame continues for 1805 nucleotides, encoding 601 residues of a polypeptide (the full length of which has not been established), followed by a 3' untranslated region of 165 nucleotides.

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232/116

We designed primers for amplification. The reported partial cDNA was screened for sequence variance in 36 unrelated individuals using the single strand conformation polymorphism (SSCP) technique as described in the methods section. Two sequence variances were identified, an A vs. G transition at nucleotide 89 and a G vs. C transversion at nucleotide 1798, both within the coding sequence. The published nucleotides are A and G, respectively. The nucleotide 1798 sequence variance alters the sense of the 599th codon (the third codon from the end of the coding sequence) to serine vs. threonine.

The frequency of KARS heterozygotes varies among the populations surveyed. The frequency of heterozygotes for the nucleotide 89 sequence variance is 19% in the 36 individuals tested. However all heterozygous individuals were either North American Whites (4/16; 25% heterozygotes), North American Blacks (1/4; 25%), or Hispanics (1/3; 33% heterozygotes). The frequency of heterozygotes for the nucleotide 1798 sequence variance is 6% in the 36 individuals tested. However all heterozygous individuals were North American Blacks (2/4; 50%) (see Target Gene Summary Table). Further study of these and other population groups will better establish the frequency of heterozygotes for these two sequence variances.

The KARS gene maps to 16q23-q24

The human KARS cDNA has been mapped to chromosome 16q22 by Nichols et al. (ref. 2) and by us. We designed primers to the 3' untranslated region of KARS and used PCR to analyze the National Institute of General Medical Sciences (NIGMS) Human/Rodent Somatic Cell Hybrid Mapping Panel #2 (see page 704 of the NIGMS 1994/1995 Catalog of Cell Lines, available from the Coriell Cell Repository, Camden, NJ). The panel consists of 24 hybrid cell lines, each monochromosomal for one human chromosome. The KARS PCR product mapped to the hybrid containing human chromosome 16. Similar results were obtained by Nichols et al., who mapped KARS

by analysis of the same NIGMS hybrid mapping panel, by PCR mapping in a chromosome 16 regional mapping panel and by fluorescence *in situ* hybridization to metaphase chromosomes. The *in situ* hybridization showed KARS maps to 16q23-q24. All mapping techniques were conclusive in showing only one locus for human KARS.

Loss of heterozygosity occurs frequently at 16q23-q24 in many cancer types. Loss of heterozygosity studies of chromosome 16q have principally focused on breast and liver cancers. In six detailed studies of breast cancer in the 16q23-q24 region LOH frequencies of 30-60% have been reported (refs 3-8). 16q22 LOH has been reported in 35-65% of liver cancers (9-13), with the average around 45%. Studies of other cancer types report 16q22 LOH in 19% of colon cancers (14), 17-27% of esophageal cancers (15,16), 37% of ovarian cancers (new ref) (17-19), 18% of prostate cancers (20) and 23% of uterine cancers (21). Cancer types not yet investigated for LOH include kidney, leukemia and lymphoma, lung, melanoma, neuroblastoma, stomach and testis.

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15 **Example 21: Ribosomal Protein S14 (RPS14) - Target Gene VARIA326**

Ribosomal protein S14 is essential for cell growth

20 Human ribosomal protein S14 (RPS14) is one of ~80 unique protein constituents of the mammalian ribosome. Many of the protein subunits of ribosomes, the protein making machines of all cells, are highly conserved throughout prokaryotic and eukaryotic evolution (1). For example, human RPS14 protein is 100% amino acid identical to hamster S14 protein, 72% identical to yeast rp59 protein and 43% identical to *E. Coli* ribosomal protein S11 (2,3). Mammalian S14 and yeast rp59 are components of the 40S ribosomal subunit while *E. coli* S11 is part of the corresponding bacterial S30 subunit. Thus human RPS14 is a ribosomal component fixed early in evolution.

25

There are many antibiotics and eukaryotic cell poisons that act by inhibiting ribosome function (reviewed in ref. 4). One such drug is emetine, which inhibits protein translation by interacting with the eukaryotic RPS14 subunit to prevent elongation

factor dependent translocation of peptidyl-tRNAs bound to eukaryotic ribosomes in vitro (4).

Chinese hamster ovary (CHO) cell lines resistant to emetine have been shown to contain mutant RPS14 loci (also referred to as the EMTB locus) (5). Such lines have been used to investigate the effects of mutant RPS14 on ribosome function (5-8). Human-CHO cell hybrids are emetine-sensitive, indicating that the EMTB/RPS14 mutation is recessive in CHO cells. This is apparently because arrest of protein synthesis in half of ribosomes blocks translation of all polysomic mRNAs by blocking any functional ribosomes upstream of frozen mutant ribosomes. RPS14 appears to contribute to the structural integrity of the 40S subunit: 40S subunits containing mutant S14 protein are more easily dissociable in high ionic strength wash buffers (9). Ribosomal subunit genes are coordinately expressed in all cells and ribosomal proteins constitute a large fraction of the cell mass in all cell types.

The human RPS14 gene has sequence variances

Rhoads et al. reported the sequence of the human RPS14 gene and cDNA (3). The cDNA contains a 33 nucleotide 5' untranslated region, a 453 nt coding region and a 60 nt 3' untranslated region (including 12 nt of polyA). We undertook a systematic search for DNA sequence variance in the cDNA of RPS14 by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed using the sequence of Rhoads et al. (GENBANK accession M13934, M13641; see ref. 3). SSCP analysis revealed 1 sequence variance, and subsequent DNA sequence analysis confirmed an A vs. G transition at nucleotide 183 of the coding sequence. (This change was noted as a difference between the cDNA and genomic sequences in ref. 3.)

As shown in the Target Summary Table, both alleles were detected in all major

populations surveyed, including North American Whites, North American Blacks, Hispanics, Chinese and Japanese.

The human RPS14 gene maps to chromosome 5q23-q33

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Dana and Wasmuth (11) used Chinese hamster/human somatic cell hybrids to map the RPS14 gene (designated EMTB) to 5q23-5q35. Later Nakamichi et al. (12) placed the RPS14 gene on the segment 5q23-q33 using similar techniques.

10

Chromosome band 5q23-q33 is a site of frequent loss of heterozygosity. There have been many studies of LOH on 5q, particularly the 5q21-q22 region where the Adenomatous Polyposis Coli (APC) tumor suppressor gene lies. The most extensively studied cancers are those of the gastrointestinal tract, lung and ovary. The available data on the 5q23-q33 region just distal to APC (where RPS14 lies), suggests that LOH occurs in this region at a frequency of ~30% in cervical cancer (13), 20-40% in colon cancer (14,15), 30-50% in ovarian cancer (16,17), 38% in stomach cancer (18) and 23% in testicular cancer (19). There is also evidence for LOH in head and neck, lung, and liver cancers.

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Example 22: Eukaryotic Initiation Factor 5A (eIF-5A) - Target Gene VARIA351

Initiation Factor 5A is essential for cell growth

Human Initiation Factor 5A (eIF-5A), formerly named Initiation Factor 4D, is an 18-kD protein which promotes formation of the first peptide bond in *in vitro* translation systems - hence the name 'initiation factor' (1,2); however, the full physiological role of eIF-5A is not understood. Inhibition of eIF 5A formation blocks proliferation in all tested cell types (3); the presence of functional eIF 5A has been shown to correlate with the onset of DNA replication (4) - perhaps due to eIF 5A dependent translation of mRNAs encoding proteins necessary for DNA replication (3), and eIF-5A is an essential co-factor for HIV-1 Rev protein (5).

eIF 5A is an unusual protein: one of its lysine residues (amino acid 50) is modified by transfer and hydroxylation of the butylamino-group from the polyamine spermidine to form hypusine, a post translational modification unique to eIF 5A. All of the biological activities of eIF 5A are abrogated in the absence of the hypusine modification, as demonstrated by pharmacological inhibition of hypusine formation in human cell lines (3) and by site directed mutagenesis of the modified lysine residue in the yeast enzyme (6). There are two enzymes responsible for hypusine formation, one of which, deoxyhypusyl hydroxylase, can be inhibited with the drug mimosine (3), providing a convenient pharmacological inhibitor of eIF 5A formation.

The genome of the yeast *Saccharomyces cerevisiae* encodes two eIF 5A genes. Disruption of one (form A) slows growth, disruption of the other (form B) arrests growth and strains with both forms disrupted are non-viable (6). The yeast A form substitutes for human eIF 5A in the mammalian methionyl-puromycin synthesis assay (6), while the human gene complements eIF 5A disrupted yeast (7). eIF 5A is a highly conserved protein, with counterparts in archaee, bacteria and eukaryotes. The yeast proteins are ~63% identical to the human protein (6).

The human eIF 5A gene and mRNA have sequence variances

Smit-McBride, et al. reported the sequence of a human cDNA encoding eIF-5A (8) and Koettnitz et al. (8) later reported the sequence of the active eIF 5A gene, which contains three introns (GenBank accession U17969). A composite sequence made from the cDNA and genomic versions is 1309 nucleotides long and contains a 5' untranslated region of 145 nucleotides, a 462 nt coding region and a 702 nt 3' untranslated region (see annotated sequence). We undertook a systematic search for DNA sequence variance in the cDNA of eIF 5A by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed for amplification. SSCP analysis revealed 2 sequence variances, and subsequent DNA sequence analysis confirmed an A vs. G transition at nucleotide 623 and a T vs. C transition at nucleotide 1012, both in the 3' untranslated sequence.

Neither sequence variance affects the protein coding sequence, however nucleotide 623 is one nucleotide away from a splice acceptor site at position 622, and could therefore be targeted by an oligonucleotide intended to abrogate splicing in an allele specific manner. The second exonic nucleotide (+2 position) of a splice acceptor site is not highly conserved, nonetheless the A vs. G transition at nucleotide 623 may affect the mechanics of splicing.

As shown in the Target Summary Table, both alleles were detected in all major populations surveyed, including North American Whites, North American Blacks, Hispanics, Arabs, Indians and Japanese, except only the nucleotide 1012 variance was detected in the four Chinese surveyed. The overall frequency of heterozygotes was 37% for the nucleotide 623 sequence variance and 52% for the nucleotide 1012 sequence variance.

The human eIF 5A gene maps to chromosome 17p13-p12

Steinkasserer et al. (1995) mapped the eIF 5A gene to 17p13-p12 by fluorescence *in situ* hybridization (9). Three eIF 5A pseudogenes were mapped to 10q23, 17q25 and 19q13.

Chromosome band 17p13-p12 is a site of frequent loss of heterozygosity. There have been many studies of LOH on 17p, particularly the 17p13 region where the p53 tumor suppressor gene maps. Virtually all cancer types have been surveyed for LOH in this area, with particularly extensive studies of breast, colon, ovarian, and stomach cancers. These studies report LOH in approximately 40-60% of breast cancers (10-18), 50-70% of colon cancers (19-25), 25-75% of ovarian cancers (26-30), 20-60% of stomach cancers (31-34), 20-50% of brain cancers (35,36), 45-70% of esophageal cancers (37), 35-65% of non-small cell lung cancers (38,39) and 100% of small cell lung cancers, 15-50% of cervical cancers, 30-80% of head and neck cancers, 20-60% of liver cancers, over 50% of sarcomas and 10-30% of a variety of other cancer types.

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15 **Example 23: Replication Protein A, 32 kDa Subunit (RPA32) - Target Gene VARIA402**

The human RPA32 gene encodes a protein essential for cell survival

20 Replication Protein A (RPA; also known as Replication Factor A, Activator 1, Single Strand Binding Protein or SSB) is a heterotrimeric protein which participates in DNA replication, homologous recombination and nucleotide excision repair (1-3). The evidence that RPA is an essential protein comes from *in vitro* and *in vivo* data.

25 DNA replication is essential for cell proliferation, as discussed above for RPA70.

The best studied function of RPA32 is in DNA replication. Because of the complexity of DNA replication in higher eukaryotic genomes, the small genome of the papovavirus SV40 has been used as a model system to study DNA replication in human cell extracts. In the 1980s several research groups

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developed cell free systems to study DNA replication using SV40 chromosomes as templates (4-8). An effort to identify the minimal set of factors required for DNA replication led to the discovery of RPA. Subsequent work proved that each of the three subunits of RPA is essential for DNA replication (9,10). This was proved in several ways, including by using antibodies to various constituents of the replication complex. Anti-RPA32 antibodies inhibit DNA replication, providing clear *in vitro* evidence for the essential function of this subunit of RPA in human DNA replication (10).

The yeast *S. cerevisiae* has a trimeric replication protein A which is structurally and functionally homologous to the human protein. It consists of three subunits similar in size to the human subunits. All three yeast subunits have been disrupted and each disruption produces non-viable yeast (9).

The human RPA32 gene and mRNA are polymorphic.

The published cDNA for the 32 kD subunit of Replication Protein A is 1512 nucleotides long and includes a 5' untranslated segment of 77 nucleotides, followed by a protein coding region of 810 nucleotides and a 3' untranslated region of 625 nucleotides (10). We undertook a systematic search for DNA polymorphism by analysing the RPA32 cDNA from 36 unrelated individuals using the single strand conformation polymorphism technique (described in the methods section). Primers were designed using the sequence of Erdile et al. (GenBank accession J05249; see ref. 10). SSCP analysis revealed 2 variances, one of which was sequenced. Sequencing revealed a G vs. A transition at nucleotide 40 of the 5' untranslated region. Four of 36 individuals were heterozygotes, all of them Caucasians. Thus the allele frequency is 25% (4/16) in North American Whites, while no heterozygosity was detected in other populations (see Target Summary sheet).

The RPA32 gene maps to chromosome 1p35

The gene for RPA32 was mapped to chromosome band 1p35 by *in situ* hybridization, somatic cell hybrid analysis and yeast artificial chromosome mapping (11,12). Only one locus was detected by all methods.

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Chromosome band 1p35 is a site of frequent loss of heterozygosity. The short arm of chromosome 1 is comparatively well investigated for allele loss, especially in breast and colon cancers. Studies of the 1p35 region show LOH in 15-40% of breast cancers (13,14), ~50% of gliomas (a brain cancer subtype) (15), 20-70% of colon cancers (16,17), ~50% of stomach cancers (18), ~20% of lung cancers (19) and 10-30% of ovarian cancers. High frequency LOH has been detected in several uncommon cancers such as pheochromocytoma (50-80%) and neuroblastoma (~50%).

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Example 24: Replication Protein A, 70 kD subunit (RPA70) - Target Gene VARIA401

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The human RPA70 gene encodes a protein essential for cell survival

Replication Protein A (also known as Replication Factor A, Activator or Single Strand Binding protein [SSB]) is a heterotrimeric protein which participates in DNA replication, homologous recombination and nucleotide excision repair (1-3). The evidence that RPA is an essential protein comes from *in vitro*, *in vivo* and evolutionary data.

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DNA replication is essential for cell proliferation, and a variety of antiproliferative drugs act, at least in part, by inhibiting DNA replication. Such drugs include nucleotide analogs that block DNA polymerases, such as 2',3' dideoxy NTPs and 3' deoxy ATP (cordycepin); inhibitors that bind to or modify DNA such as intercalating agents, DNA crosslinking drugs or alkylating agents, and inhibitors that bind to polymerases and replication proteins such as topoisomerase inhibitors like the epipodophyllotoxins, which prevent DNA unwinding necessary for replication (and transcription) and antibiotics which bind to polymerases such as arylhydrazino-pyrimidines.

The best studied function of RPA70 is in DNA replication. Because of the complexity of DNA replication in higher eukaryotic genomes, the small genome of the papovavirus SV40 has been used as a model system to study DNA replication in human cell extracts. In the 1980s several research groups

developed cell free systems to study DNA replication using SV40 chromosomes as templates (4-8). These studies, in seeking to identify the minimal set of factors required for DNA replication, led to the discovery of replication protein A. Subsequent work proved that each of the three subunits of RPA is essential for DNA replications. This was proved in several ways, including by using antibodies to various constituents of the replication complex. These antibodies are effectively inhibitors of RPA70. Anti-RPA70 antibody mediated abrogation of DNA replication provides clear *in vitro* evidence for the essential function of RPA70 in human DNA replication (10). The yeast *S. cerevisiae* has a trimeric replication protein A which is structurally and functionally homologous to the human protein. It consists of three subunits similar in size to the human subunits. The yeast 70 kDa subunit is 31% identical and 75% similar (including conserved amino acids) to its human counterpart (1). All three yeast subunits have been disrupted and each disruption produces non-viable yeast. The yeast 70 kD protein is also a single stranded DNA binding protein.

Single stranded DNA binding proteins (SSBs) are required for DNA replication in a wide variety of organisms, including bacteriophage, bacteria and some DNA viruses of higher eukaryotes. Recently the crystal structure of the DNA binding domain of human RPA was solved and found to be remarkably similar in three dimensional shape to the bacteriophage single stranded DNA binding proteins Pf3 and gene V from f1 phage.

The human RPA70 gene, mRNA and protein have sequence variances

The published cDNA for the 70 kD subunit of Replication Protein A is 2393 nucleotides long and includes a 5' untranslated segment of 69 nucleotides, followed by a protein coding region of 1848 nucleotides and a 3' untranslated region of 476 nucleotides (1). We undertook a systematic search for DNA polymorphism by

analyzing the RPA70 cDNA from 36 unrelated individuals using the single strand conformation polymorphism technique (described in the methods section). Primers were designed using the sequence of Erdile et al. (GenBank accession M63488; see ref. 1). SSCP analysis revealed 5 variances, and subsequent DNA sequence analysis of those variances led to identification of four additional variances. SSCP revealed the variances at nucleotides 81 (G vs. A), 1120 (A vs. G), 1674 (T vs. C), 2050 (T vs. C) and 2297, where an insertion/deletion variance of one C nucleotide was observed (8 vs. 9 C's in a row). In the course of sequencing around the nucleotide 2297 polymorphism an additional variance was detected at nucleotide 2341 (A vs. G). Also, while sequencing additional Swedish individuals around nucleotide 1120 two new variances were observed at nucleotides 1124 and 125 (both C vs. T). Finally, in three individuals sequenced for the 2050 variance we noted a difference from the published sequence at nucleotide 2046: we detect 3 T's while the published clone shows just two. This difference may represent another insertion/deletion polymorphism. Five of the nine detected variances are in the coding sequence while four are in the 3' untranslated region.

The frequency of heterozygotes for the five SSCP positive variances ranged from 25-42% among the 36 individuals tested. The small number of individuals genotyped for the other four variances precludes definitive assessment of heterozygosity rates. Some of the polymorphisms appear to occur more commonly in certain racial or ethnic groups (see Target Summary sheet for details). For example, only one of the variances (nt 1674) was detected in Japanese individuals. In general, higher levels of polymorphism were detected in North American Whites than in other groups. The nucleotide 1120 polymorphism, for instance, was heterozygous in 9/36 individuals overall (25%), but in 8/16 North American Whites (50%).

The RPA70 cDNA encodes a 616 amino acid protein. The nucleotide 1120 and 1124 variances result in amino acid substitutions at residues 351 and 352, the former an alanine-threonine exchange (approximately 50% of caucasians are heterozygotes) and

the latter a serine-phenylalanine exchange (rare in the populations tested). In the recently published crystal structure of the DNA binding segment of RPA70 (amino acids 181-422) it is possible to place residue 351 in the second of two tandemly arrayed DNA binding domains (domain B; see ref. 10). Domain B extends from residue I305 to N402, thus the variant residue 351 is in the middle. The published structure is a co-crystal of RPA70 amino acids 181-422 complexed to octadeoxycytosine. Several RPA70 residues contact the oligonucleotide (Figure 4 of ref. 11), including amino acids K343 and T359, which lie 8 residues away from the polymorphism in either direction. Modeling the two variant forms of the protein using the atomic coordinates deposited in the Protein Data Bank (1JMC) should clarify the structural consequences of the alanine-threonine variance. Residue 351 lies in the center of a 50 amino acid segment of the protein that is relatively poorly conserved between yeast and man: 11 of the 50 residues are identical and 25 more are conservative substitutions. Towards the C terminus there is strong conservation: starting 25 residues C-terminal of the polymorphism, 27 of the next 37 residues are identical between yeast and man. Towards the N terminus there is ~30% conservation. Both yeast and human 70 kD RPA subunits contain putative C4-type zinc finger motifs at positions ~480-500.

The RPA70 gene maps to chromosome 17p13.3

The gene for RPA70 has been mapped to chromosome band 17p13.3 by *in situ* hybridization (12). Only one locus was detected.

Chromosome band 17p13.3 is a site of frequent loss of heterozygosity. RPA70 lies just telomeric to the TP53 tumor suppressor gene which is located in cytogenetic band 17p13.1. This region of chromosome 17 is extremely well investigated for allele loss. In general, studies report LOH in approximately 40-60% of breast cancers (13-21), 50-70% of colon cancers (22-28), 25-75% of ovarian cancers (29-33), 20-60% of stomach cancers (34-37), 20-50% of brain cancers (38,39), 45-70% of esophageal cancers (40),

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35-65% of non-small cell lung cancers (41,42) and 100% of small cell lung cancers, 15-50% of cervical cancers, 30-80% of head and neck cancers, 20-60% of liver cancers, over 50% of sarcomas and 10-30% of a variety of other cancer types.

5 *Assays developed for RPA: Protein and DNA contacts*

Human cDNAs encoding all 3 subunits (70, 34 and 11 kD) of RPA have been cloned and expressed in *E. coli* and in insect cells via baculovirus vectors. The bacterially expressed 70 kDa protein is indistinguishable from its purified human counterpart immunologically and in several functional assays (see Table below). There is good evidence that the 70 kD subunit of RPA interacts with a number of different molecules. A partial list would include the 34 and 11 kD subunits of RPA, DNA, the xeroderma pigmentosum damage recognition and endonuclease proteins XPA and XPG, and DNA polymerase α -primase. These experimentally proven contacts (and almost certainly others) may constrain the topology of the protein in ways that have implications for inhibitor design. In summary a broad array of assays exists to screen for small molecule inhibitors of RPA (possibly including modified nucleotides), that act via competitive, allosteric or protein-protein blocking mechanisms.

15 **Table 4**

20 **Assays and reagents available for RPA inhibitor screening**

ASSAY	RPA 70 kD, Assay Systems	
	Purified Human Protein	Purified Bacterial or Baculovirus Protein
Immunoreactivity	X	X
Single stranded DNA binding	X	X
DNA Polymerase alpha primase	X	X

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DNA strand exchange	X	X
Nucleotide excision repair	X	X
Support SV40 Replication	X	X

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25 **Example 25: RNA Polymerase II, 220-kD subunit (RPOL2A) - Target Gene VARIA500**

The human RPOL2A gene encodes a protein essential for cell survival

DNA-dependent RNA polymerase II (also known as RPB1 or POLR2A), a complex

multisubunit enzyme, is responsible for the transcription of mRNA from all protein coding genes.

5 RNA polymerases are found in all cellular organisms. The subunit structure of RNA polymerases is highly conserved in eukaryotes. RNA polymerase acts in concert with as many as 50 other proteins in gene transcription (reviewed in ref. 1). See refs. 2 and 3 for a review of basal transcription by RNA polymerase II and recent progress in identifying and purifying transcription factors and cloning the genes that encode them.

10 Several subunits of *S. cerevisiae* RPOL2A have been disrupted, always resulting in non-viable yeast.

15 A variety of inhibitors of RNA polymerase are cytotoxic drugs, such as actinomycin D, which intercalates into double stranded DNA and blocks the movement of RNA polymerase; rifampicin binds the β subunit of *E. coli* RNA polymerase and blocks initiation of transcription. The best studied specific inhibitor of eukaryotic RPOL2A, however, is the potent mushroom toxin - amanitin, a cyclic octapeptide which binds with high affinity ($K_d \sim 10^{-9}$ M) to RPOL2A. Several mutations conferring resistance to α -amanitin have been characterized and they all map to the RPOL2A protein coding sequence.
20 Recently α -amanitin binding has been shown to trigger specific degradation of RPOL2A (4).

25 Damage to actively transcribed DNA is preferentially repaired by the transcription-coupled repair (TCR) system. TCR requires RNA pol II, but the mechanism by which repair enzymes preferentially recognize and repair DNA lesions on PolB II-transcribed genes is incompletely understood.

The human RPOL2A gene and mRNA have sequence variances

Wintzerith et al. and later Mita et al. cloned and sequenced the complete human gene

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for RPOL2A (5, 6); the deduced amino acid sequences are identical. The RPOL2A gene contains 29 exons and spans about 32 kb of DNA. The cDNA sequence we evaluated is 6732 nucleotides long (see Annotated RPOL2A Sequence) and contains a 5' untranslated region of 386 nucleotides, a 5910 nucleotide coding region specifying 1970 amino acids, and a 436 nucleotide 3' untranslated region (see annotated sequence). We undertook a systematic search for DNA sequence variance in the cDNA of RPOL2A by analyzing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed for amplification. SSCP analysis revealed 10 sequence variances, and subsequent DNA sequence analysis confirmed a G vs. A transition at nucleotide 857, a C vs. T transition at nucleotide 1260, a C vs. T transition at nucleotide 1346, a C vs. T transition at nucleotide 1544, a C vs. T transition at nucleotide 1847, a C vs. T transition at nucleotide 2678, a C vs. T transition at nucleotide 3059, a C vs. T transition at nucleotide 3827, a T vs. C transition at nucleotide 6466 and a T vs. C transition at nucleotide 6557. The former seven sequence variances are in coding sequence and the latter two are in the 3' untranslated sequence. Only one of the ten sequence variances alters the protein coding sequence: the nucleotide 1260 alleles encode arginine (common) or cysteine (rare) at amino acid 292. Only 2/36 individuals surveyed are heterozygotes (6%), however both are North American Whites (2/16 = 12.5%) so further investigation of this population is required. The prevalence of heterozygotes for the other sequence variances varies from 3% to 50%, with 6 sequence variances above 22% (see RPOL2A Target Summary Sheet). The 6 common sequence variances are widely prevalent among all or nearly all the tested populations.

The human RPOL2A gene maps to chromosome 17p13.105

The human RPOL2A gene was initially assigned to the distal portion of the short arm of chromosome 17 (17pter-p12) by *in situ* hybridization and Southern analysis of DNA from human/rodent somatic cell hybrids (7, 8). Subsequent somatic cell hybrid studies narrowed the assignment to 17p13.105-p12 [vanTuinen and Ledbetter (1987)], which

was later confirmed by *in situ* hybridization to 17p13 (9).

Chromosome band 17p13.1 is a site of frequent loss of heterozygosity There have been many studies of LOH on 17p, particularly the 17p13.1 region where the p53 tumor suppressor gene maps. Virtually all cancer types have been surveyed for LOH in this area, with particularly extensive studies of breast, colon, ovarian, and stomach cancers. These studies report LOH in approximately 40-60% of breast cancers (10-18), 50-70% of colon cancers (19-25), 25-75% of ovarian cancers (26-30), 20-60% of stomach cancers (31-34), 20-50% of brain cancers (35,36), 45-70% of esophageal cancers (37), 35-65% of non-small cell lung cancers (38,39) and 100% of small cell lung cancers, 15-50% of cervical cancers, 30-80% of head and neck cancers, 20-60% of liver cancers, over 50% of sarcomas and 10-30% of a variety of other cancer types.

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Example 26: TATA Associated Factor 30 kD subunit (TAF2H) - Target Gene VARIA 520

The human TAF2H gene encodes a component of the transcriptional apparatus

Transcription initiation by RNA polymerase II requires the assembly of a complex of

basic transcription factors which include TFIIA, TFIIB, TFIID, TFIIIE, TFIIF, TFIIG/TFIIJ and TFIIH/BTF2 into a preinitiation complex (1,2). TFIID is the first factor to contact the promotor, and subsequent assembly of the transcription complex is dependent on TFIID binding. TFIID is a 700-750 kD multiprotein complex which includes TATA binding protein (TBP) and between eight and 13 TBP-associated factors (TAFs) ranging from 250 to 17 kDa. The TAFs have been shown necessary to reconstitute activation of transcription *in vitro*, leading to the hypothesis that some TAFs link transcription activation domains to the basal transcription complex. The TFIID complex also supports transcription from TATA-less promoters, while TBP fails to do so. Therefore TAFs may also contribute to formation of stable initiation complexes by interacting directly with DNA (2). Conditional temperature sensitive Chinese hamster mutants of another TAF, TAFII250, were detected because, at the non-permissive temperature, DNA synthesis was inhibited leading to arrest of cell division at the G1 phase (3,4). Transfection of a human TAFII250 gene relieved the block at the non-permissive temperature. Thus an essential role has been proven for TAFs in mammalian cells.

A gene (TAF2H) encoding the 30 kDa human TAF protein (TAFII30) was cloned and its functional properties examined by Jacq, et al. (5). The protein was shown to be present in a subset of TFIID complexes and to mediate transcriptional activation by a specific region of the estrogen receptor. Estrogen mediated transcriptional activation could be abrogated by adding an antibody against TAFII30. TAFII30 was not required for basal transcription or for transcription activation by VP-16. It is likely that TAFII30 is required for transcriptional activation by a variety of other transactivating proteins, and is therefore essential for cell proliferation or cell survival.

The human TAF2H gene and mRNA have sequence variants

A human TAF2H cDNA has been cloned and sequenced (5). It encodes a cDNA of 756 nucleotides including a 5' untranslated region of 17 nucleotides, a 657 nucleotide

coding region specifying 218 amino acids, and an 82 nucleotide 3' untranslated region (GenBank accession U13991; see annotated TAF2H cDNA sequence). (Note that the numbering of the sequence in ref. 5 differs slightly from that in the GenBank accession.) We undertook a systematic search for DNA variance in the cDNA of TAF2H by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed for amplification. SSCP analysis revealed 1 polymorphism, and subsequent DNA sequence analysis confirmed a G vs. A transition at nucleotide 554 (nt 556 of the sequence in ref. 3) of the coding sequence. This variance does not alter the protein coding sequence. Eight of 36 individuals surveyed are heterozygotes (22%). The variance occurs in North American Whites (3/16 = 19%), North American Blacks (2/4) and Hispanics (3/3).

The human TAF2H gene maps to chromosome 11p15.5-p15.2 The human TAF2H cDNA has been mapped to 11p15.5-p15.2 by fluorescent *in situ* hybridization (6). There appears to be a single TAF2H locus. *Chromosome band 11p15-p14 is a site of frequent loss of heterozygosity*

There have been many studies of LOH on 11p, particularly the 11p15 and 11p13 segments where the Beckwith-Weidemann syndrome and WT1 genes reside. As a result there are many studies of LOH in 11p15.5, particularly focusing on breast, cervix, kidney, liver, lung, ovarian, stomach and testicular cancers. These studies show that the 11p15.5 band of chromosome 11 is frequently reduced to one copy (7-24). For example, LOH occurs in approximately 13-33% of breast cancers (7-9), 14-42% of cervical cancers (10), 0-50% of liver cancers (11,12), 0-80% of lung cancers (13-15), 18-54% of ovarian cancers (14,15), 0-71% of stomach cancers (18) and 0-50% of testicular cancers (19,20). Other studies show that 11p15.5 LOH may also be frequent in bladder cancer (21), esophageal cancer (22), some leukemias (23) and sarcomas (24). Many deletions in the 11p15.5 region span relatively short chromosomal segments (2 - 10 megabases; see ref. 13).

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Example 27 - cDNA synthesis

In order to analyze an essential gene for sequence variances, it is generally useful to have a cDNA(s) containing the coding sequence for further sequencing or amplification purposes. cDNAs for some genes are available, however, in some cases it is useful to synthesize the cDNA *de novo*. Methods for obtaining cDNA are known to those skilled in the art, as are methods for sequencing or amplifying the cDNA or portions thereof. An example of a useful cDNA production protocol is provided below, however, as recognized by those skilled in the art, other specific protocols can also be used.

cDNA Production

** Make sure that all tubes and pipette tips are RNase-free. (Bake them overnight at 100°C in the vacuum oven to make them RNase-free.)

1 Add the following to a RNase-free 0.2 ml micro-amp tube and mix gently:

24 ul water (DEPC treated)

12 ul RNA (1 µg/ul)

12 ul random hexamers(50 ng/ul)

2 Heat the mixture to 70°C for ten minutes.

3 Incubate on ice for 1 minute.

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4 Add the following:

16 ul 5 X Synthesis Buffer

8 ul 0.1 M DTT

5 4 ul 10 mM dNTP mix (10 mM each dNTP)

4 ul SuperScript RT II enzyme

Pipette gently to mix.

5 Incubate at 42°C for 50 minutes.

6 Heat to 70°C for ten minutes to kill the enzyme, then place it on ice.

10 7 Add 160 ul of water to the reaction so that the final volume is 240 ul.

8 Use PCR to check the quality of the cDNA. Use primer pairs that will give a
~800 base pair long piece. See "PCR Optimization" for the PCR protocol.

15 The following chart shows the reagent amounts for a 20 ul reaction, a 80 ul
reaction, and a batch of 39 (which makes enough mix for 36) reactions:

	20 ul X 1 tube	80 ul X 1 tube	80ul X 39 tubes	
20 water	6 ul	24 ul	936	water
RNA	3 ul	12 ul		RNA
random hexamers	3 ul	12 ul	468	random hexamers
25 synthesis buffer	4 ul	16 ul	624	synthesis buffer
0.1 M DTT	2 ul	8 ul	312	0.1 M DTT
10mM dNTP	1 ul	4 ul	156	10mM dNTP
SSRT	1 ul	4 ul	156	SSRT

30

Example 28 - Variance detection by SSCP

This example describes the SSCP technique as used for the identification of sequence variances of the exemplary genes, which were then sequenced to confirm the specific base variances. One common technique currently employed in the identification of such single nucleotide differences is the single strand conformation polymorphism (SSCP) method. (originally described in Orita, *et al.*, "Rapid and Sensitive Detection of Point Mutations and DNA Polymorphisms Using the Polymerase Chain Reaction, *Genomics*, 5:874-879 (1989)) Also employed are restriction fragment length polymorphism (RFLP), heteroduplex analysis, ligase chain reaction (LCR), denaturing gradient gel electrophoresis (DGGE) (Myers, Maniatis, and Lerman, *Methods Enzymol.*, 155:501-527 (1987)) or direct nucleotide sequencing. A review of polymorphism detection techniques, including SSCP, is provided in Grompe, 1993, *Nature Genetics* 5:111-117, which includes a comparison of the commonly used methods.

The SSCP method reveals the presence of sequence variation between individuals as shifts in electrophoretic mobility, but does not show the sequence itself. Direct sequencing of DNAs with altered mobility in the SSCP assay identifies the precise nucleic acid sequence differences among the various alleles. From the nucleic acid sequence data, the amino acid sequence can be determined. One example of the use of this technique is in Pelletier *et al.*, *Cell*, 67:437-447 (1991). The single strand conformation polymorphism methodology is effective for scanning essential genes for sequence variants. It remains the standard technique in human genetics for variance detection, with numerous studies of its efficacy (>90%) and schemes for improved throughput. The SSCP method has been shown to be quite sensitive in the detection of single base changes, for example as shown in Ravnik-Glava *et al.*, 1994, *Human Mol. Genet.* 3:801-807 (human cystic fibrosis gene) and Glava & Dean, 1993, *Human Mutation* 2:404-414 (mouse α -globin gene).

A flow chart of the SSCP method as used to identify essential gene sequence variants is shown in Fig. 2 (SSCP OVERVIEW). The method involves the steps of 1) PCR

amplifying a portion of an essential gene cDNA of known sequence (labeled products),
2) selecting restriction enzymes which will produce fragments approximately 100-400
bases in length for 3 independent digestions of the PCR products, 3) heat denaturing
the digestion products, 4) running single strand digestion products on non-denaturing
5 gels, 5) identifying bands having different mobilities when compared between
individuals, thereby identifying potential sequence variants, 6) sequence at least the
region around the potential sequence variance, that region being identified by
comparison of the expected fragment sizes resulting from the digestions, 7) record the
specific location and base identity of the confirmed sequence variant, 8) calculate the
10 percent occurrence of each sequence variance for the gene as found for the sample of
the population. The method is further described in Example 2.

Single strand conformation polymorphism screening is a widely used technique for
identifying an discriminating DNA fragments which differ from each other by as little
15 as a single nucleotide. As originally developed by Orita (supra), the technique was
used on genomic DNA, however the same group showed that the technique works very
well on PCR amplified DNA as well. In the last 8 years the technique has been used
in hundreds of published papers, and the modifications of the technique have been
described in dozens of papers. The enduring popularity of the technique is due to (1)
20 a high degree of sensitivity to single base differences (>90%) (2) a high degree of
selectivity, measured as a low frequency of false positives, and (3) technical ease.
SSCP is almost always used together with DNA sequencing because SSCP does not
directly provide the sequence basis of differential fragment mobility. The basic steps
of the SSCP procedure are described below and summarized in Fig. 2 in flow chart
25 form.

Because the intent of our SSCP screening was to identify as many target gene
variances as practically possible, we developed a protocol designed to look at a
relatively large number of individuals (36) with a high degree of redundancy, so as to
minimize both the false negative and false positive rates.

The 36 individuals examined are reasonably representative of most of the worlds major populations. The racial or geographic origin of the 36 cell lines is detailed in the Target Summary Tables (Figure 5). All cell lines are EBV immortalized lymphoblastoid cells obtained from the Coriell Cell Repository (Camden, NJ), which includes the racial/ethnic/geographic background of cell line donors in its catalog. The cell lines were also selected for their rapid growth rates. In several cases a panel of cDNAs isolated from French Canadians was used instead, or in addition to, the Coriell panel.

SSCP was used to analyze cDNAs (rather than genomic DNAs) because in many cases the full genomic sequence of the target gene is not available, however, the technique is also applicable to genomic sequences. To produce cDNA requires RNA. Therefore each of the 36 cell lines was grown to mass culture and RNA was isolated using the acid/phenol protocol, sold in kit form as TRIAZOL™ by Life Technologies (Gaithersburg, MD). The unfractionated RNA was used to produce cDNA by the action of a modified Maloney Murine Leukemia Virus Reverse Transcriptase, purchased in kit form from Life Technologies (SUPERScript II™ kit). The reverse transcriptase was primed with random hexamer primers to initiate cDNA synthesis along the whole length of the RNAs. This proved useful later in obtaining good PCR products from the 5' ends of some genes.

Material for SSCP analysis was prepared by PCR amplification of the cDNA in the presence of one ³²P labeled dNTP (usually ³²P dCTP). Usually the concentration of nonradioactive dCTP was dropped from 200 uM (the standard concentration for all four dNTPs) to about 100 uM, and ³²P dCTP was added to a concentration of about 0.1-0.3 uM. This involved adding a 0.3- 1 ul (3-10 uCi) of ³²P cCTP to a 10 ul PCR reaction. All radioactivity was purchased from DuPont/New England Nuclear.

The customary practice is to amplify about 200 base pair PCR products for SSCP, however, we found that it was preferable to amplify about 0.8-1.4 kb fragments and

then use several cocktails of restriction endonucleases to digest those into smaller fragments of about 0.1-0.4kb, aiming to have as many fragments as possible between .15 and .3 kb. The digestion strategy had the advantage that less PCR was required, reducing both time and costs. Also, we routinely performed three different digests on each sample (for all 36 cDNAs), and then ran each of the digests separately on SSCP gels. This had the effect of increasing the redundancy of our method, lessening both the false negative and false positive rates. For example: a site of variance might lie within 2 bases of the end of a fragment in one digest, and as a result not affect the conformation of that strand; the same variance, in a second or third digest, would likely lie in a location more prone to affect strand folding, and therefore be detected by SSCP.

After digestion, the radiolabeled PCR products were diluted 1:5 by adding formamide load buffer (80% formamide, 1X SSCP gel buffer) and then denatured by heating to 90°C for 10 minutes, and then allowed to renature by quickly chilling on ice. This procedure (both the dilution and the quick chilling) promotes intra- (rather than inter-) strand association and secondary structure formation. The secondary structure of the single strands influences their mobility on nondenaturing gels, presumably by influencing the number of collisions between the molecule and the gel matrix (i.e., gel sieving). Even single base differences consistently produce changes in intrastrand folding sufficient to register as mobility differences on SSCP.

The single strands were then resolved on two gels, one a 5.5% acrylamide, 0.5X TBE gel, the other an 8% acrylamide, 10% glycerol, 1X TTE gel. The use of two gels provides a greater opportunity to recognize mobility differences. Both glycerol and acrylamide concentration have been shown to influence SSCP performance. The gel apparatus we use (from Owl Scientific, MA) allows 108 samples to be loaded per gel. Since all 36 samples are routinely digested with three different endonuclease mixes there are 108 samples to be analyzed for each PCR product. By routinely analyzing three different digests under two gel conditions (effectively 6 conditions), and by

looking at both strands under all 6 conditions, we achieve a 12-fold sampling of each base pair of cDNA.

5 All of the sequence variances described in this disclosure were determined by DNA cycle sequencing of ^{32}P labeled PCR products using the femtomole DNA cycle sequencing kit from Promega (WI) and the instructions provided with the kit. Fragments were selected for DNA sequencing based on their behavior in the SSCP assay.

10 **Example 29 - Variance detection by using T4 endonuclease VII mismatch cleavage method**

15 The enzyme T4 endonuclease VII is derived from the bacteriophage T4. T4 endonuclease VII is used by the bacteriophage to cleave branched DNA intermediates which form during replication so the DNA can be processed and packaged. T4 endonuclease can also recognize and cleave heteroduplex DNA containing single base mismatches as well as deletions and insertions. This activity of the T4 endonuclease VII enzyme can be exploited to detect sequence variances present in the general population.

20 The following are the major steps involved in identifying sequence variations in a candidate gene by T4 endonuclease VII mismatch cleavage:

- 25
1. Amplification by the polymerase chain reaction (PCR) of 400-600 bp regions of the candidate gene from a panel of DNA samples. The DNA samples can either be cDNA or genomic DNA and will represent some cross section of the world population.
 2. Mixing of a fluorescently labeled probe DNA with the sample DNA. Heating

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and cooling the mixtures causing heteroduplex formation between the probe DNA and the sample DNA.

3. Addition of T4 endonuclease VII to the heteroduplex DNA samples. T4 endonuclease will recognize and cleave at sequence variance mismatches formed in the heteroduplex DNA.
4. Electrophoresis of the cleaved fragments on an ABI sequencer to determine the site of cleavage.
5. Sequencing of a subset of PCR fragments identified by T4 endonuclease VI to contain variances to establish the specific base variation at that location.

A more detailed description of the procedure is as follows:

A candidate gene sequence is downloaded from an appropriate database. Primers for PCR amplification are designed which will result in the target sequence being divided into amplification products of between 400 and 600 bp. There will be a minimum of a 50 bp of overlap not including the primer sequences between the 5' and 3' ends of adjacent fragments to ensure the detection of variances which are located close to one of the primers.

Optimal PCR conditions for each of the primer pairs is determined experimentally. Parameters including but not limited to annealing temperature, pH, $MgCl_2$ concentration, and KCl concentration will be varied until conditions for optimal PCR amplification are established. The PCR conditions derived for each primer pair is then used to amplify a panel of DNA samples (cDNA or genomic DNA) which is chosen to best represent the various ethnic backgrounds of the world population or some designated subset of that population.

One of the DNA samples is chosen to be used as a probe. The same PCR conditions used to amplify the panel are used to amplify the probe DNA. However, a

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fluorescently labeled nucleotide is included in the deoxy-nucleotide mix so that a percentage of the incorporated nucleotides will be fluorescently labeled.

5 The labeled probe is mixed with the corresponding PCR products from each of the DNA samples and then heated and cooled rapidly. This allows the formation of heteroduplexes between the probe and the PCR fragments from each of the DNA samples. T4 endonuclease VII is added directly to these reactions and allowed to incubate for 30 min. at 37 C. 10 ul of the Formamide loading buffer is added directly to each of the samples and then denatured by heating and cooling. A portion of each
10 of these samples is electrophoresed on an ABI 377 sequencer. If there is a sequence variance between the probe DNA and the sample DNA a mismatch will be present in the heteroduplex fragment formed. The enzyme T4 endonuclease VII will recognize the mismatch and cleave at the site of the mismatch. This will result in the appearance of two peaks corresponding to the two cleavage products when run on the ABI 377
15 sequencer.

Fragments identified as containing sequencing variances are subsequently sequenced using conventional methods to establish the exact location and sequence variance.

20 **Example 30 - Identification of Sequence Variances by Informatics-based analysis of gene-sequence databases**

In addition to and/or in conjunction with the molecular biology based approaches for identifying sequence variances in genes, particularly in essential genes, such sequence
25 variances can be identified by analysis of public and/or private genetic sequence databases. Such information can be either genomic or cDNA sequence information.

The data base analysis process includes the following major steps:

1.

1. capture of homologous sequences of a particular gene from data bases. It is preferable to obtain a large number of independent sequences of a particular gene

5

2. analysis of collected sequences of a particular gene to identify authentic sequence variances. This step involves the discrimination of authentic sequence variances, which are sequence variances which actually exist in the population, from sequencing errors and artifacts. It is expected that about 0.1-0.3% of the bases will occur as true variances, while the frequency of sequencing artifacts is expected to be 1-3%. This discrimination utilizes the expected frequencies of occurrence of specific types of nucleotide sequence changes. Such information includes the characteristic frequency of specific transitions and transversions and of the characteristic frequency of deletions and insertions in authentic variations. It uses the frequency of occurrence of known types of sequencing artifacts such as single base insertions or deletions adjacent to repeated C or G nucleotides. Additional information for such discrimination is provided if particular putative authentic variations are observed in multiple independently derived sequences of the gene.

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An implementation of this sequence variance identification process utilizes a reference sequence of an essential gene. Preferably, the reference sequence is a high quality sequence, meaning that there is a low frequency of occurrence of sequencing errors or artifacts. The second step is the retrieval of allelic sequences of that essential gene from available databases such as the BLAST server, the UNIGENE database, or other such sequence database. Such allelic sequences need not be complete, but are preferably long enough to ensure that they are in fact allelic sequences. The third step involves alignment analysis to identify and tabulate sequence differences between the different available sequences. An algorithm for such analysis is the Smith-Waterman local alignment algorithm. Use of an algorithm of this type involves a series of pair-

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wise alignments of each retrieved sequence with the reference sequence. The fourth step involves analysis of the observed sequence differences and assignment of a probability that each sequence difference represents an authentic variance. This analysis utilizes program filters which are combined in a weighted fashion to determine a final probability. Such program filters include comparison of the observed difference with common mutational changes and sequencing errors, a weighting of the reliability of a particular retrieved sequence based on the total number of differences observed, a weighting based on the location within a retrieved sequence where a change was observed and a significant weighting based on the observance of a particular difference in multiple independently derived retrieved sequences.

Using such an implementation, a database analysis with respect to a particular reference sequence produces a list of putative authentic sequence variances and a probability for each of those variances that the sequence difference is an authentic variance. As described above, the probability is obtained through the use of a series of weighted program filters and thus these filters are modified to produce optimal authentic variance discrimination.

Example 31 - Antiproliferative effects of variance specific inhibition of RPA70

This example describes experiments showing the practicality and utility of variance-specific inhibition of essential genes for cancer therapy. Specifically, this example describes *in vitro* experiments showing the design and production of variance-specific oligonucleotides for antisense inhibition of variant alleles of the essential Replication Protein A, 70 kDa subunit (RPA70) for inhibition of RPA70 mRNA, and the use of these oligonucleotides to inhibit cell proliferation and to reduce the number of cells in a variance-specific manner.

Variance-specific inhibition and cell killing with antisense oligonucleotides against

RPA70

These experiments with RPA70 illustrate the feasibility of each of the steps for development of a variance specific inhibitor:

5 Select candidate target gene essential for cell survival or proliferation. As described above, RPA is essential for replication in prokaryotic and eukaryotic cells, mitochondria, phage, viruses and in *in vitro* (SV40) replication systems. The protein is a heterotrimer required for loading DNA polymerase onto the DNA template during cell replication. The 70 kDa subunit, RPA70, is a single strand binding protein that
10 mediates the interaction of RPA with DNA. Without this protein, the replication complex does not associate with DNA and the replication of DNA does not occur.

Confirm chromosome location and LOH frequency. RPA70 is encoded by a single gene locus on chromosome 17p13.3, immediately adjacent to the p53 gene at 17p13.1.
15 LOH involving chromosome band 17p13.3 has been documented in 50-70% of colon, lung, breast, and ovarian cancers. LOH at this locus also occurs in other cancers. The inventor as confirmed LOH involving RPA 70 in breast, colon, lung and other cancers.

Identify common variances in the normal population. We have identified five common
20 variances in the RPA70 gene (Figure 8). The most common occurs in 42% of the normal population. One variance alters the amino acid sequence and is present in 25% of the normal population (44% of Caucasians). This variance occurs within the active DNA binding domain (discussed below). These variances are described in the description above and in Fig. 1.

25 Demonstrate antiproliferative effects due to inhibition of candidate gene. The inventor has shown that inhibition of RPA70 in T24 bladder carcinoma cells with an antisense oligonucleotide reduces cell number. This effect is comparable to treatment of these cells with antisense oligonucleotide against *ras*, previously shown to have antitumor

effects *in vitro* and *in vivo* (Figure 9).

Design variance-specific inhibitor. Variance specific antisense oligonucleotides were designed to differentially inhibit the two variant forms of RPA70. Experiments were performed using tumor cell lines that are homozygous for each form of the target gene. Figure 10 shows inhibition of mRNA levels in Mia Paca II cells by the 13085 oligonucleotide which matches the variance in these cells. In contrast, in T24 cells (and A549 cells, see below) the 12781 oligonucleotide matches the target gene and inhibits mRNA levels. In both cell lines neither the control oligonucleotide differing by one base (13085 in T24 cells and 12781 in Mia Paca II cells) nor a random-sequence oligonucleotide control (13706) inhibit mRNA levels to the same extent as the matched oligonucleotide.

Figure 10 demonstrates that the RPA 70 mRNA can be specifically down regulated in an allele-specific manner. However, the 13085 oligomer used also has a small effect on the level of the unmatched RNA. In order to increase the discrimination we altered the structure of the targeting oligomer, 13085. The results are shown in Figure 11. By shortening the oligomer we retain its ability to down-regulate its matched target RNA (Mia Paca II cells, right half of Figure 11). Strikingly, however, this alteration dramatically altered the ability of this oligomer to down-regulate the mismatched variant RNA T24 cells, left half of Figure 11. The reciprocal regulation by oligomer 12781 was augmented by altering transfection conditions. These data suggest that even simple changes to the rudimentary "first generation" chemistry and transfection techniques can have significant effects in enhancing the ability of the oligomers to recognize and down regulate specific mRNAs.

Achieve variance-specific antiproliferative effects in cancer cells. Cell proliferation in each cell line, determined by BrdU incorporation, was suppressed to a greater degree by the matched oligonucleotide than by the controls differing by one base (Figure 12).

Cell proliferation in A549 cells was inhibited by oligomer 12781 to a greater degree than by oligomer 13085. Cell proliferation in Mia Paca 11 cells was inhibited more by oligomer 13085.

5 Additional studies were performed to characterize the antiproliferative effect in A549 cells (12781 genotype). A dose response curve demonstrates inhibition of BrdU incorporation by the matched oligonucleotide (12781) at concentrations 8-fold lower than the oligonucleotide with one base mismatch (13085) (Figure 13).

10 Cell survival was measured by staining cells with Sulforhodamine B dye 72 hours after treatment with oligonucleotides. Dose dependent reductions in cell number were observed in cells treated with the matched oligonucleotide (12781) but not with an oligonucleotide containing the one base mismatch (13085) (Figure 14). In contrast, in
15 Mia Paca II cells, more cell killing was observed with the 13085 oligonucleotide than with the 12781 oligonucleotide (Figure 15). The oligonucleotides used in these studies have not been optimized for achieving allele-specific effects. Oligonucleotides using advanced chemistries can be utilized to optimize the potency and provide greater discrimination between variant targets at lower levels.

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Example 32 - variance specific inhibition of essential genes

This example describes experiments showing the practicality and utility of variance-specific inhibition of essential genes for cancer therapy including RNA Pol II, and ribonucleotide reductase. Specifically, this example describes *in vitro* experiments
25 showing the design and production of variance-specific oligonucleotides for antisense inhibition of variant alleles of the essential Ribonucleotide Reductase (RR), the design and production of variance-specific oligonucleotides against RR, and the use of these oligonucleotides to inhibit RR mRNA in a variance-specific manner.

Variance-specific inhibition of Ribonucleotide Reductase.

Ribonucleotide Reductase (RR) is an essential gene of nucleoside metabolism. Inhibitors of this function are known to be cell lethal. Two variances were discovered at position 2410 and 2419. Oligonucleotides were synthesized to a sequence spanning these two variations. In one case the oligomer targeted the GnnnnnnnnA variation (oligomer Varia 2410GA or RR2410GA) and in the other case the oligomer targeted the AnnnnnnnnG variant (oligomer Varia 2410AG or RR2410AG). In Mia Paca II cells which contain the GnnnnnnnnA variance, the RR2410GA antisense oligomer dramatically knocked down the level of RR mRNA. However, the oligomer targeting the other variance, oligomer Varia 2410AG, had little to no effect on the level of mRNA (Figure 16). The reciprocal regulation was demonstrated in MDA-MB 468 cells which express the other variance, AnnnnnnnnG (Figure 17). In these cells Varia 2410AG dramatically lowered the level of RR mRNA. In contrast, Varia 2410GA had no effect on the level of mRNA. These data taken together, are another example of allele-specific targeting of gene expression. We are also determining the effect of down regulating RR gene expression on cellular growth.

Example 33 - variance specific inhibition of essential genes using advanced oligonucleotide chemistries.

This example describes experiments showing the practicality and utility of variance-specific inhibition of essential genes for cancer therapy. Specifically, this example describes *in vitro* experiments showing the design and production of variance-specific oligonucleotides for antisense inhibition of variant alleles of the essential Glutamyl/prolyl tRNA Synthetase (EPRS), the design and production of variance-specific oligonucleotides against EPRS, and the use of these oligonucleotides to inhibit EPRS mRNA in a variance-specific manner.

Glutamyl-prolyl-tRNA synthetase (EPRS) is an essential gene, required for the synthesis of both glutamic acid tRNA and proline tRNA. Without EPRS protein synthesis is blocked. Two variances were discovered in this gene at positions 2963 and 2969 in the cDNA. We have demonstrated variance-specific inhibition of this gene with antisense oligonucleotides exploiting several different types of chemistry.

The experiments described above with RPA70 and RR utilized phosphorothioate chemistry. This chemistry was developed to achieve greater stability *in vivo*, and this compound has been used in several successful clinical trials. Phosphorothioates, however have low affinity for the RNA target, and, consequently, relatively lower specificity. We have achieved improved variance-specific inhibition using alternative chemistries. Specifically, we have synthesized hybrid oligonucleotides that contain both phosphorothioate and nucleotides with higher affinities. These hybrids contain "wings" consisting of six nucleotides with a 2' sugar modification (ethoxy-methoxy radical at the 2' position) and either a phosphorothioate or phosphodiester backbone. Between the "wings" is a 8 nucleotide sequence of phosphorothioates that overlaps the variance. (In these constructs the 5' position of cytosine has been methylated.) As shown in Figure 18, variance specific inhibition is observed with the conventional phosphorothioates. Greater inhibition of target mRNA is observed using the hybrid chemistries at lower doses. Inhibition by the matched hybrid oligomer, 14977, occurs at approximately 50-100 nM. The effect is extremely oligomer-specific. The mismatched oligomer, 14971, has no effect on mRNA levels at concentrations as high as 400 nM (Figure 19).

Example 34 - *in vivo* cancer therapy using oligonucleotides

This example describes reported *in vitro* and *in vivo* data on the treatment of cancer in animal models using antisense oligonucleotides against c-raf, showing the expected

correlation between *in vitro* suppression of mRNA and cell proliferation with oligonucleotides, and *in vivo* anticancer activity.

5 *In vitro* evidence for inhibition of mRNA by antisense oligonucleotides and inhibition of cell proliferation is commonly used to predict *in vivo* effects on tumors. This is exemplified by the publication by Monia et al (Nature Medicine, Volume 2 Number 6, June 1996) who demonstrated anticancer effects using oligonucleotides against C-raf kinase. *In vitro* treatment of human tumor cells with appropriate phosphorothioate antisense oligomers led to specific inhibition of C-raf kinase gene expression and
10 subsequent decrease in cellular proliferation, IC₅₀=50-100nM. Administration of C-raf antisense oligomers to nude mice having a tumor burden derived from these cells significantly inhibited tumor growth *in vivo*, IC₅₀= 0.06-0.6 mg/kg. Remarkably, the investigators were able to show that the anti-C-raf oligomers down-regulated the level of C-raf kinase mRNA *in vivo* by assaying mRNA levels in cells removed from the
15 tumor.

Example 35 - *in vivo* cancer therapy by oligonucleotide inhibition of ras

20 This example describes reported *in vivo* data showing an anticancer effect using an allele-specific inhibitor for suppression of mutant H-ras. Schwab *et al* (*Proc. Nat. Acad. Sci. USA* 91:10460-464, Oct 1994) demonstrated antitumor effects of an antisense oligonucleotide specific for the mutant ras in animal models. In these experiments HBL100 cells were transformed with the RAS oncogene. *In vitro* studies
25 demonstrated that the RAS mRNA could be specifically down-regulated by a nanoparticle conjugated phosphodiester antisense oligomer. Only the transforming RAS mRNA was targeted by the oligomer. The normal cellular RAS mRNA, differing by a single base, was not affected by the antisense oligomer. The decrease in RAS expression was associated with a decrease in the growth rate of the cells. The

transformed HBL100 cells were injected into nude mice to form tumors; following subcutaneous injection of nanoparticle-conjugated phosphodiester antisense oligomers, Schwab et al measured both a decrease in targeted tumor weight and volume. Specificity for tumor cell growth correlated well with the *in vitro* data having a 5-fold differential between antisense and control groups.

The authors of this paper are proceeding with clinical trial of these oligonucleotides for the treatment of cancer, demonstrating the potential clinical utility of these methods.

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Example 36. Variance detection by DGGE

This example describes denaturing gradient gel electrophoresis (DGGE), a technique used for the identification of DNA sequence variances in genomic DNA, cDNA or in PCR products amplified from genomic DNA or cDNA. The DGGE method was originally described by Fischer and Lerman (Two Dimensional Electrophoretic Separation of Restriction Enzyme Fragments of DNA. Methods in Enzymology, vol. 68: 183-191, 1979; DNA Fragments Differing by Single Base-Pair Substitutions are Separated in Denaturing Gradient Gels: Correspondence with Melting Theory. Proc. Natl. Acad. Sci. U.S.A. 80:1579, 1983) and has been improved since then by many investigators. See, for example: Myers, et al., Mutation Detection by PCR, GC-Clamps, and Denaturing Gradient Gel Electrophoresis, pp. 71-88 in Erlich, H.A., editor: PCR Technology: Principles and Applications for DNA Amplification, Stockton Press, New York, 1989; Myers, et al., Detecting Changes in DNA: Ribonuclease Cleavage and Denaturing Gradient Gel Electrophoresis, in Davies, K.E., editor: Genomic Analysis: A Practical Approach, IRL Press Ltd., Oxford, 1988, pp. 95-139; E.S. Abrams and V.P. Stanton Jr., Use of Denaturing Gradient Gel Electrophoresis, pp. 71-104 in Lilley, D.M.J. and Dahlberg, J.E., editors: DNA Structures. Part B: Chemical and Electrophoretic Analysis of DNA, Methods in

Enzymology, volume 212, Academic Press, 1992; .) Descriptions of current applications of the technique can be found in

5 The basic principal of DGGE involves the creation of a gradient of denaturant in a gel, which is then used to resolve double stranded DNA (or RNA) fragments on the basis of conformational differences associated with strand melting. The denaturant can be chemical (as in DGGE, where a gradient of formamide and urea is typically used) or thermal (as in a related technique called thermal gradient gel electrophoresis, or TGGE, where a gradient of heat is used). To obtain conditions where double stranded DNA
10 is close to melting, DGGE gels are immersed in a heated bath of electrophoresis buffer, while TGGE gels have a fixed concentration of chemical denaturant.

15 As a double stranded DNA molecule migrates through a DGGE gel from a low concentration of denaturant at the origin to higher concentrations of denaturant toward the end of the gel it eventually reaches a level of denaturant that will cause partial melting. (Some design of DNA molecules is often necessary to assure that the partial melting will occur as desired; see below.) The concentration of denaturant required to melt a given DNA segment is highly sensitive to sequence differences in the DNA, including changes as subtle as a single nucleotide substitution. Partially melted DNA
20 fragments move through gels at a much slower rates than their fully duplex counterparts. Thus two DNA fragments differing at a single nucleotide can be distinguished on the basis of their gel position after an appropriate period of electrophoresis: the fragment with the more stable structure (resulting from, for example, a G:C base pair in place of an A:T pair) will travel further in the gel than its
25 less stable counterpart, because it will encounter the concentration of gradient required to melt it (and consequently dramatically retard or nearly stop its movement) at a point further along in the gel.

The DGGE method reveals the presence of sequence variation between individuals as

shifts in electrophoretic mobility, but does not show the sequence itself. Direct sequencing of DNA fragments (from different individuals) with altered mobility in the DGGE assay will reveal the precise sequence differences among them (see example 37, Variance Detection by DNA Sequencing). From the nucleic acid sequence data, the amino acid sequence can be determined and any amino acid differences can be identified.

The DGGE method is suitable for analysis of restriction enzyme digested genomic DNAs, as initially described by Lerman and co-workers (*supra*) and later extended (Gray; M. Detection of DNA Sequence Polymorphisms in Human Genomic DNA by Denaturing Gradient Blots, American Journal of Human Genetics, 50: 331-346, 1992). DGGE is equally suitable for analysis of cloned DNA fragments or DNA fragments produced by PCR. The analysis of cloned fragments or PCR fragments has the advantage that non-natural sequences, rich in G and C nucleotides can easily be added to the 5' ends (either flanking the cloning site or at the 5' ends of PCR primers). Such DNA fragments have very stable double stranded segments, called GC clamps, at one or both ends. The GC clamps alter the melting properties of the fragments, and can be designed so as to insure melting of the inter-primer segment of the PCR product at a lower temperature than the clamps, thereby optimizing the detection of sequence differences (see Myers *et alia*, *supra* and Myers *et alia*, Nearly All Single Base Substitutions in DNA Fragments Joined to a GC Clamp Can be Detected by Denaturing Gradient Gel Electrophoresis. Nucleic Acids Research 13: 3131, 1985). GC clamps can be rationally designed for any specific DNA fragment of known sequence by use of a computer program (MELT87, written by L. Lerman) that accurately predicts melting behavior based on analysis of primary sequence. When GC clamps are used correctly, the DGGE method is highly efficient at detecting DNA sequence differences. Not only are nearly 100% of differences detected, but the false positive rate is essentially zero. (Abrams, E.S., *et alia*, Comprehensive Detection of Single Base Changes in Human Genomic DNA Using Denaturing Gradient Gel

Electrophoresis and a GC Clamp. Genomics 7: 463-475, 1990.) Recently methods for increasing the throughput of DGGE have been developed, based on multiplex PCR.

The steps in carrying out DGGE with GC clamps are:

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1. *Design DNA fragments with optimal melting behavior.* Select oligonucleotide primers, using GC clamps as necessary, to produce a single melting domain over the length of the sequence to be analyzed. (It may be necessary to divide the sequence into overlapping fragments to achieve this goal.) Design of primers and simulated analysis of fragments can be performed with the computer program described by Lerman. (Lerman, L.S. and Silverstein, K. Computational Simulation of DNA Melting and its Application to Denaturing Gradient Gel Electrophoresis. Methods in Enzymology 155: 482-501, 1987.) The output of the program is the melting map of the fragment, from which it will also be possible to determine the optimal range of denaturant in the gradient and the approximate electrophoresis time for fragments to reach the point of melting in the gradient.

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2. *Amplify the fragment by PCR.* Procedures for optimizing PCR are briefly described in other examples and are well known in the art. Template DNA samples can either be cDNA or genomic DNA and will typically be drawn from a panel of unrelated individuals.

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3. *Pour a denaturing gradient gel.* Briefly, make up two gel solutions containing the desired beginning and end concentrations of denaturant. The gel solutions are generally made up by mixing "0%" and "100%" denaturant stock solutions, where the 0% stock consists of 7% acrylamide in Tris-acetate EDTA (TAE) electrophoresis buffer, and the 100% stock is also 7% acrylamide in TAE, plus 40% formamide by volume and 7 molar urea. Equal volumes of the two solutions (e.g. twelve milliliters of each solution) are poured into the two chambers of a gradient maker (usually between 20 and 40% denaturant in the upstream chamber and 60 to 80% in the lower

25

one) immediately after addition of ammonium persulfate and TEMED for acrylamide polymerization. Open the stopcock of the gradient maker and pour the gradient gel. Usually gels are .75 to 1 mm in thickness, and gel combs that form 10-30 wells are used. With commercially available apparatus multiple gradient gels can be poured simultaneously. Suitable apparatus is sold by several vendors, including the BioRad (Hercules, CA) Dcode system and the C.B.S. Scientific DGGE system.

4. *Place the gel in a heated bath of electrophoresis buffer.* Gels are electrophoresed at elevated temperature which, together with the denaturant, brings the DNA fragments to their melting point. Gels are often run at 60°C in 1X TAE buffer, with constant recirculation of buffer to the upper buffer chamber. Once the gel has been placed in the heated tank and allowed to equilibrate it can be loaded. Multiple gels can be run simultaneously in the same tank with the apparatus listed above.

5. *Load and run gel.* Usually enough PCR product from each sample is loaded on the gel so that samples can be detected by a simple DNA staining procedure; use of radioactivity, dyes or hybridization procedures can thereby be avoided. At least 100 mg of each sample should be loaded, but preferably over 200 ng. Gel running conditions can be estimated from the output of the MELT87 program, however empirical adjustment will often be necessary. Usually a voltage of ~80 to 200V is applied for periods of 5-20 hours, depending on the characteristics of the fragments being analyzed.

6. *Stain and analyze gel.* After electrophoresis gels are stained with ethidium bromide, SYBR Green, silver or some other procedure. The location of PCR products produced with the same primer pairs should be compared. Altered location, and usually the appearance of two or more bands instead of one, signify the presence of DNA sequence differences. (The reason for more than two bands from a diploid sample is that during the terminal cycle of heating and cooling of the PCR

step heteroduplexes are formed between the maternally and paternally inherited alleles. If those alleles differ in sequence, the heteroduplexes will have mispaired nucleotides at the sites of difference. As a result the heteroduplexes will be less stable than either of the homoduplex species, and will consequently melt and be retarded in the gel at a lower concentration of denaturant. Altogether one may see four bands in such samples: two reciprocal heteroduplexes and two homoduplexes.) The specific pattern of fragments in each lane constitutes a signature for a specific nucleotide change.

7. *Sequence DNA fragments with altered mobility.* Examples of all different signatures should next be analyzed by DNA sequencing to identify the base difference(s) accounting for altered mobility in the gradient gel. See example 37 for a description of this procedure and the subsequent steps of recording the sequence variances and analyzing their frequency and structural and functional consequences.

Example 37: Variance detection by sequencing.

Sequencing by the Sanger dideoxy method or the Maxim Gilbert chemical cleavage method is widely used to determine the nucleotide sequence of genes. Presently, a worldwide effort is being put forward to sequence the entire human genome. The Human Genome Project as it is called has already resulted in the identification and sequencing of many new human genes. Sequencing can not only be used to identify new genes, but can also be used to identify variations between individuals in the sequence of those genes.

The following are the major steps involved in identifying sequence variations in a candidate gene by sequencing:

1. Amplification by the polymerase chain reaction (PCR) of 400-700 bp regions of the candidate gene from a panel of DNA samples. The DNA samples can either be cDNA or genomic DNA and will represent some cross section of the world population.
- 5 2. Sequencing of the resulting PCR fragments using the Sanger dideoxy method. Sequencing reactions are performed using fluorescently labeled dideoxy terminators and electrophoresed on an ABI 377 sequencer or its equivalent.
3. Analysis of the resulting data from the ABI 377 sequencer using software programs designed to identify sequence variations between the different
10 samples analyzed.

A more detailed description of the procedure is as follows:

15 A candidate gene sequence is downloaded from an appropriate database. Primers for PCR amplification are designed which will result in the target sequence being divided into amplification products of between 400 and 700 bp. There will be a minimum of a 50 bp of overlap not including the primer sequences between the 5' and 3' ends of adjacent fragments to ensure the detection of variances which are located close to one of the primers.

20 Optimal PCR conditions for each of the primer pairs is determined experimentally. Parameters including but not limited to annealing temperature, pH, $MgCl_2$ concentration, and KCl concentration will be varied until conditions for optimal PCR amplification are established. The PCR conditions derived for each primer pair is
25 then used to amplify a panel of DNA samples (cDNA or genomic DNA) which is chosen to best represent the various ethnic backgrounds of the world population or some designated subset of that population.

PCR reactions are purified using the QIAquick 8 PCR purification kit (Qiagen cat#

28142) to remove nucleotides, proteins and buffers. The PCR reactions are mixed with 5 volumes of Buffer PB and applied to the wells of the QIAquick strips. The liquid is pulled through the strips by applying a vacuum. The wells are then washed two times with 1 ml of buffer PE and allowed to dry for 5 minutes under vacuum.

5 The PCR products are eluted from the strips using 60 ul of elution buffer.

The purified PCR fragments are sequenced in both directions using the Perkin Elmer ABI Prism™ Big Dye™ terminator Cycle Sequencing Ready Reaction Kit (Cat# 4303150). The following sequencing reaction is set up: 8.0 ul Terminator Ready

10 Reaction Mix, 6.0 ul of purified PCR fragment, 20 picomoles of primer, deionized water to 20 ul. The reactions are run through the following cycles 25 times: 96°C for 10 second, annealing temperature for that particular PCR product for 5 seconds, 60°C for 4 minutes.

15 The above sequencing reactions are ethanol precipitated directly in the PCR plate, washed with 70% ethanol, and brought up in a volume of 6 ul of formamide dye. The reactions are heated to 90°C for 2 minutes and then quickly cooled to 4°C. 1 ul of each sequencing reaction is then loaded and run on an ABI 377 sequencer.

20 The output for the ABI sequencer appears as a series of peaks where each of the different nucleotides, A, C, G, and T appear as a different color. The nucleotide at each position in the sequence is determined by the most prominent peak at each location. Comparison of each of the sequencing outputs for each sample can be examined using software programs to determine the presence of a variance in the

25 sequence. One example of heterozygote detection using sequencing with dye labeled terminators is described in Pui-Yan Kwok *et. al.* (Pui-Yan Kwok, Christopher Carlson, Thomas D. Yager, Wendy Ankener, and Deborah A. Nickerson, *Genomics* 23, 138-144 (1994)). The software compares each of the normalized peaks between all the samples base by base and looks for a 40% decrease in peak height and the concomitant

appearance of a new peak underneath. Possible variances flagged by the software are further analyzed visually to confirm their validity

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Example 38. Loss of heterozygosity.

Loss of chromosomes or segments of chromosomes in disease cells results in loss of alleles in the disease cells compared to normal diploid cells. Such allele losses are a common occurrence in cancer, where they have been documented in over 1,500 publications in the past 14 years. More recent work has documented the occurrence of allele loss in other proliferative diseases. Several cytogenetic and molecular techniques have been developed to measure chromosome losses. The molecular techniques are preferable for identification of allele loss because they also show which allele is lost, and are therefore best suited to provide the information needed to implement the present invention.

In order to measure chromosome loss using molecular techniques it is necessary to be able to distinguish the paternally and maternally inherited copies of a given chromosome. DNA variances allow the two copies of a given chromosome to be distinguished because different alleles can be resolved electrophoretically. The standard method for analyzing allele loss in cancer is to compare tumor cell DNA with normal cell DNA, either in a Southern blot or using PCR based techniques. A patient's tumor DNA is said to be "informative" for allele loss only at loci where the patient's normal cells are heterozygous. When such heterozygous loci are examined in tumor cells often only one allele is detected. Such tumor cells have lost the heterozygous state which characterizes all normal somatic cells of the patient, hence the term loss of heterozygosity (LOH).

Several effective molecular procedures have been developed to measure LOH. These procedures have been applied most extensively to cancer tissues, however the same methods are effective in the study of nonmalignant diseases such as atherosclerotic plaques and endometriosis. The main steps are:

5

1. *Identify DNA variances at or near the locus to be investigated for LOH.*

10

LOH usually affects large segments of DNA, ranging from several megabases to an entire chromosome. As a result, accurate estimation of LOH at a specific locus can be obtained by measuring the frequency of LOH at neighboring polymorphic markers on the same chromosome, or more preferably on the same chromosome arm, or most preferably within several 10-20 megabases of the locus. However, to precisely measure LOH at a specific locus requires a variance at the locus. Different types of variances have been used to study LOH, including single nucleotide polymorphisms (SNPs), specifically SNPs that alter restriction endonuclease cleavage sites, called RFLPs. (For details of this approach see Vogelstein, B., et al., Allelotype of colorectal carcinomas. *Science* 244: 207-211, 1989). Also short tandem repeat polymorphisms (STRPs), including di-, tri- and tetranucleotide repeat polymorphisms have been used to measure LOH. (For details of this procedure see Jones and Nakamura, Deletion Mapping of Chromosome 3p in Female Genital Tract Malignancies Using Microsatellite Polymorphisms. *Oncogene* 7: 1631-1634, 1992.) Procedures for identifying variances are described in Examples 28, 29, 30 and 36.

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2. *Prepare DNA from paired normal and disease tissue samples from patients being studied.*

Before preparing genomic DNA from tumor tissue it is important to assess tumor cell purity and viability, using microscopic examination of frozen sections if necessary. If embedded pathological specimens are being analyzed tumor cell purity can be

assessed by examining histologic sections before selecting areas for cell isolation and DNA purification. (See Johnson, et al., Direct Molecular Analysis of Archival Tumor Tissue for Loss of Heterozygosity, BioTechniques 19:190-191, 1995, and references therein for description of techniques for purifying tumor cell DNA from archival pathology samples.) Areas of necrosis and extensive admixture of normal and tumor tissue should be avoided. For Southern blotting ~5-10 ug of genomic DNA is required for each sample being analyzed. For PCR based methods as little as 5 to 10 ng of genomic DNA is sufficient; much less will suffice if two successive rounds of PCR amplification are used.

3. *Determine genotype in the normal and disease tissues using a quantitative or semi-quantitative procedure that allows the amount of each allele to be measured. Compare the ratio of alleles in the normal tissue to the ratio in the tumor tissue*

In order to show LOH at a given locus it is necessary to establish that the patient is constitutionally heterozygous at the locus. Thus DNA from normal tissue must be tested, either before or in parallel with tumor tissue DNA. A variety of methods can be used for quantitation of signal from the two alleles. If the alleles are compared on a Southern blot then signal in the bands corresponding to the two alleles can be counted by radioactive or nonradioactive techniques (see Ausubel, et al., Current Protocols in Molecular Biology, John Wiley & Sons). One method employs phosphor technology using a Molecular Dynamics PhosphorImager with ImageQuant software to measure signals. If the alleles are compared after PCR amplification then DNA sequencing can provide accurate quantitation of allele ratios. See, for example, Goldsborough and Kornberg, Allele-Specific Quantification of Drosophila Engrailed and Inverted Transcripts, Proc. Natl. Acad. Sci. U.S.A. 91:12696-12700, 1994.

Using highly variable markers distributed across the genome a comprehensive map of LOH can be assembled for a specific cancer type. Such data sets have been termed allelotypes. Separate studies are necessary for different cancer (or other disease) types

as the patterns of LOH differ significantly in different diseases.

Other techniques that have been used to detect allele loss in cancer include Comparative Genomic Hybridization (CGH) and Representation Difference Analysis (RDA) however these methods are more complex than the Southern blot or PCR based techniques. Chromosome loss can also be detected cytogenetically. Mitelman (Catalog of Chromosome Aberrations in Cancer. Wiley-Liss, New York, 1995.) has compiled a catalog of over 10,000 published karyotypes of cancer cells which documents chromosome deletions as well as other changes.

Example 39. Small molecule inhibitors of variant sequences:

Methylguanine Methyltransferase (MGMT)

Gene VARIA 1534

The methylguanine methyltransferase gene is essential for cell growth or survival in the presence of alkylating agents

Methylguanine methyltransferase (MGMT) is a nuclear protein that repairs alkylating agent damage, specifically alkylation of the O6 position of guanine bases in genomic DNA. MGMT acts as a suicide protein in removing methyl or alkyl groups from guanine and covalently binding them to cysteine 145 of MGMT. The protein is subsequently degraded; it does not act as an enzyme. O6-benzylguanine is an inhibitor of MGMT that mimics the natural substrate, alkylated DNA; transfer of the benzyl group to cysteine 145 of MGMT inactivates the protein. Concurrent administration of O6-benzylguanine and an alkylating agent such as carmustine (BCNU) or lomustine (CCNU) renders tumor cells more sensitive to the toxic effects of the nitrosoureas by inactivating MGMT and thereby inhibiting the tumor cells ability to repair alkylated

DNA. MGMT is thus a conditionally essential gene in the presence of nitrosoureas and other alkylating agents. The conditional essentiality of MGMT has been demonstrated in mice. Animals homozygous for disrupted MGMT genes are more than ten times as sensitive to alkylating agents as normal mice. The relative sensitivity has been measured as the LD50, the dose required to kill 50% of treated animals. (Tsu-
5 Suzuki, T., et al. Targeted disruption of the DNA repair methyltransferase gene renders mice hypersensitive to alkylating agent. *Carcinogenesis* 17: 1215-1220, 1996.) O6-benzylguanine is being developed as a chemosensitizing agent (with alkylating agents) for treatment of human cancer. This treatment regimen is not specific for cancer cells.

10 In a cancer patient with two alternative functional MGMT alleles in normal tissues and LOH at 10q23 resulting in only one copy of MGMT in cancer cells, an allele specific inhibitor of MGMT could be used to specifically sensitize cancer cells to the action of alkylating agents. Treatment would consist of the administration of the appropriate
15 allele specific inhibitor (directed to the one allele remaining in cancer cells) plus an alkylating agent. The tumor cells would be unable to effectively repair the alkylating agent induced DNA damage, while the uninhibited allele in normal cells would be able to function. Thus normal cells, including sensitive normal cell populations such as bone marrow stem cells, would be able to tolerate higher doses of alkylating agents
20 than cancer cells.

The MGMT gene and encoded protein are polymorphic

25 Four variances in human MGMT have been discovered by the inventors or reported in the literature, including three variances that affect the protein sequence. There is a C/T variance at nucleotide 255 (11% heterozygotes among 36 individuals surveyed) which does not affect the encoded protein. There is a second C/T variance at nt. 346 which results in a L84F amino acid variance (5% heterozygotes among 36 individuals surveyed). There is an A/G variance at nt. 523 which results in a I143V amino acid

variance (24% heterozygotes among 36 individuals surveyed). This variance occurs only two residues from the active site cysteine at 145. A fourth variance, G/A has been reported in the Japanese population at codon 160, GGA vs. AGA, resulting in a glycine vs. arginine amino acid variance. Fifteen percent of 40 Japanese individuals studied were heterozygotes for this variance. (Imai, Y., et al. A polymorphism at codon 160 of human O6-methylguanine-DNA methyltransferase gene in young patients with adult type cancers and functional assay. *Carcinogenesis* [London] 16:2441-24445, 1995.)

Allele specific inhibitors of MGMT

Two of the amino acid variances in MGMT, at residues 143 and 160, are near the active site of the protein. Substantial work has already been done to characterize the functional consequences of the residue 160 glycine/arginine variance. Studies of MGMT kinetics and activity have shown that the 160arginine allele is at least 20 fold more resistant to O6 benzylguanine inactivation, measured as an increase in the ED50 and or as a reduction in the production of guanine from O6-benzyl[8-3H] guanine. The 160gly and 160arg forms of MGMT were nearly equal in alkyltransferase activity in an assay that measured repair of O6-methylguanine in methylated DNA. These results demonstrate variance-specific effects of a small molecule, O6-benzylguanine, on normal (non-mutant) alleles of the conditionally essential MGMT gene. (Edara, S., et al. Resistance of the human O6-alkylguanine-DNA alkyltransferase containing arginine at codon 160 to inactivation by O6-benzylguanine. *Cancer Research* 56: 5571-5575, 1996)

Administration of O6-benzylguanine to patients who are heterozygous for the variance in their normal cells, and contain only the alternative form of the gene with a glycine residue at position 160 in their cancer cells, together with methylating or chloroethylating agents, will specifically sensitize cancer cells to the cytotoxic effects of the alkylating agents without increasing toxicity to normal cells which, since they

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232/116

contain the O6-benzylguanine resistant 160arginine form of the protein, will continue to repair alkylated DNA.

5 There is no published data concerning the residue 143 variance, however the proximity of this variance to the active site - both in the primary sequence and upon inspection of the three dimensional structure of the bacterial AGT protein, a functional and structural homolog of human MGMT - suggests that allele specific drugs could be discovered for this variance.

10 The structural difference between 143isoleucine and 143valine is a hydrophobic methyl group. It is well known that most small molecule protein inhibitors interact via hydrophobic interactions. Favorable Van der Waals distances between hydrophobic groups of a substrate and a ligand are vital for high affinity interaction. One possible mechanism of allele specific inhibition would be to exploit the greater
15 bulk of the isoleucine by finding a small molecule that fits into the active site pocket of the valine allele but has a very unfavorable Van der Waals interaction the methyl group of the isoleucine. Other schemes based on the different size and geometry of isoleucine and valine could also be effective.

20 One approach to identification of such inhibitors would be to make small molecule libraries in which various positions of guanine are substituted with moities of appropriate size and structure. Such libraries could then be tested in various screens of MGMT activity. The two alleles (143isoleucine and 143valine, or any of the other allele pairs of MGMT described above) would be assayed in parallel.

25 Identification of molecules with allele specific inhibitory activity could be the basis for synthesis of additional libraries in which the moities that are best correlated with differential activity are further varied. Methods for the iterative design of high affinity or highly discriminating small molecule inhibitors are known in the art.

Libraries of restricted size can be screened for allele specific inhibitors using a combinatorial strategy based on known inhibitors of MGMT such as O6-benzyl-guanine. A library or libraries can be constructed in which substitutions are introduced at positions C6 and N9 which have previously been found to affect inactivation of MGMT, or at positions C2 and N8 which can be easily substituted. For example a series of 4(6)-(benzyloxy)-2,6(4)-diamino-5-(nitro or nitroso)pyrimidine derivatives and analogs in which 4(6)-benzyloxy groups were replaced with (2-, 3-, or 4 fluorobenzyl)oxy or (2-, 3-, or 4-pyridylmethyl)oxy groups have been synthesized and tested for MGMT inhibition. (Terashima I., and K. Kohda. Inhibition of human O6-alkylguanine-DNA alkyltransferase and potentiation of the cytotoxicity of chloroethylnitrosourea by 4(6)-(Benzyloxy)-2,6(4)-diamino-5-(nitro or nitroso)pyrimidine derivatives and analogues. *J Med Chem* 41: 503-508, 1998.) Substitutions at N7 have been found to be detrimental in general (Moschel, R.C. et al & Pegg, A. E., *J. Med. Chem.* 35: 4486-4491, 1992).

Combinatorial libraries can be constructed according to a published procedure (Norman, T. C. et al., A Structure-Based Library Approach to Kinase Inhibitors. *J. Am. Chem.Soc.* 118: 7430-7431, 1996) where guanine based libraries were made by anchoring a chemically modified guanine (at C6, C2, or C8) to solid supports at C2 via a glycinamide linkage or at N9 via a hydroxyethyl linkage. Chemical reactions can be carried out to introduce a library of hydrophobic substituents of different size at positions C6, C2, or C8. Hydrophobic substituents of various bulkiness and orientation can be introduced through derivatives of O6-benzyl and O6-phenyl groups, O6-alkyl groups, N9-alkyl groups, and C2-amino-alkyl groups.

Libraries constructed as above can be screened for MGMT activity in several types of assays. Methods for bacterial expression and purification of human MGMT protein have been described (see Edara, et al., cited above). Both allelic forms of MGMT could be screened for repair of alkylated or methylated DNA by measuring transfer of tritium from a tritium labelled (methylated) DNA substrate in the

presence of various concentrations of library compounds for various times.

Alternatively, library compounds could be tritiated and MGMT proteins could be screened for the rate at which they interact with (either via association or cleavage of a moiety from the compound). Other assays for MGMT activity are known in the art.

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Example 41. Clinical use of variance specific inhibitors for treating cancer

10 Inhibitors that are the object of the present invention are designed to be administered to patients who are heterozygous for the target gene, meaning that their cells normally contain two alternative copies of the gene, one that is sensitive to inhibition by said inhibitors, and one that is not sensitive to said inhibitors. It is apparent that several such inhibitors may be developed according to this invention

15 targeted to alternative alleles of a single target gene or to several different target genes. The inventors propose that a series of such inhibitors will be developed according to this invention.

The clinical use of this invention involves the steps of:

- 20 (a) testing normal cells from a patient to identify target genes that are heterozygous, present in two alternative forms.
- (b) testing biopsy tissue from a tumor or proliferative lesion to determine whether one of the two alternative forms is eliminated due to LOH.
- (c) selecting a drug for inhibition based on the presence of the sensitive allele in the
- 25 tumor and the presence of an insensitive allele in normal cells
- (d) administering said drug to the patient in an appropriate dose to inhibit the essential function in the cancer cell.

Testing of normal cells to identify heterozygosity of the target gene is performed

using conventional diagnostic methods that are known in the art. Normal cells are commonly derived from a blood sample, hair sample, or buccal smear.

Alternatively normal cells may be obtained by cultivating primary cells such as lymphoblasts or fibroblasts in vitro. The presence of two alternative alleles may be determined by methods including allele-specific hybridization with oligonucleotides containing the variant sequences and a number of non-variant nucleotides to allow differential binding to the alternative forms of the gene or other methods known in the art using purified DNA or RNA or amplified DNA or cDNA sequences.

Testing of biopsy tissue is performed by separating tumor cells or cells of the proliferative lesion to isolate a sample of cells characteristic of the proliferative lesion for analysis. This is performed by a variety of methods known in the art including manual dissection or laser assisted methods for eliminating normal cells or selecting abnormal cells. Samples of abnormal tissue, and samples of normal tissue as a control, are analyzed to identify the presence or absence of alternative forms of the target gene. The presence of two alternative alleles may be determined by methods including allele-specific hybridization with oligonucleotides containing the variant sequences and a number of non-variant nucleotides to allow differential binding to the alternative forms of the gene or other methods known in the art using purified DNA or RNA or amplified DNA or cDNA sequences.

Selection of a drug for administration will be based on clinical trial data indicating that the drug is effective in eliminating abnormally proliferating cells and causing an improvement in the patient's clinical condition for patients who have the sensitive allele of the target gene in their pathological lesion. In one aspect of this invention, the product label will describe that the drug is indicated in patients who have only a specific allele of the target gene in their lesion and an alternative allele in their normal cells. Any such drug will be indicated only for a fraction of patients having two alternative alleles of the target gene in their normal cells and LOH. The fraction of patients who may be treated with any one drug may be determined by

5 multiplying the number of patients with a given cancer times the fraction of tumors exhibiting LOH of the target gene locus times the fraction of patients who will be heterozygous. For a target gene exhibiting 50% heterozygosity in the population and a 70% fraction of LOH in a specific cancer (several such examples are shown), a single inhibitor will treat ~17% of such cancers. A second compound directed against the alternative allele would treat another 17% of said cancer. In the preferred use of this invention, a panel of such drugs will be available enabling therapy with at least one such drug in most patients.

10 Administration of the drug to the patient ration to the patient will involve conventional means such as parenteral, oral, or intratumoral administration. The route of administration will be determined separately for each inhibitor and will be based on the bioavailability of the compound to the lesion. The compound may be administered in one or more doses as a single agent or in combination with other
15 allele specific agents or conventional antiproliferative drugs or agents commonly used for the treatment of cancer or support of cancer patients.

20 **Example 42. Cell Division Cycle 25C (CDC25C) - Gene VARIA10**

Cdc25C is essential for cell growth

25 A vital regulator of cell proliferation is the protein kinase Cdc2, whose activation at the end of G2 of the cell cycle initiates mitosis. Gene disruption experiments in yeast confirm the importance of this protein, as cells lacking Cdc2 fail to progress through the cell cycle. As would be expected for such an important protein, Cdc2 activity is tightly regulated. Its activity depends on complex formation with Cyclin B, a protein that accumulates through the cell cycle and is then abruptly degraded during mitosis. Phosphorylation of Cdc2 on Tyr-15 and Thr-14 by the Wee1/Mik1

kinases maintains the Cdc2/Cyclin B complex in an inactive state until the end of G2. The dual-specificity phosphatase Cdc25C is then stimulated to dephosphorylate Cdc2 on both residues, resulting in activation of the complex. Just as Cdc2 is essential for cell growth, the regulation of its activity is essential. The best evidence for this is that the individual disruption of *cdc2*, cyclin B, *wee 1* and *cdc25* in the yeast *S. pombe* are lethal events. When *cdc25* is deleted from these cells they display a phenotype consistent with their function; they grow without dividing, becoming dramatically elongated.

The human CDC25C gene and protein have variances

The CDC25C cDNA was cloned by Sadhu *et al.* (1) (Genbank accession number M34065, GI number 181075). To determine whether CDC25 is polymorphic, VARIAGENICS scanned cDNA from 32 unrelated individuals using the T4 Endonuclease VII method, which involves the cleavage of DNA heteroduplexes followed by DNA sequencing of polymorphic regions (see description of method in examples). A transversion at nucleotide 1099 (G or C) was identified (nucleotide numbering is from reference 1). This results in an amino acid difference at residue 297, with G encoding glycine and C encoding arginine. Overall, 9.4% of individuals analyzed are heterozygous. The rate of heterozygosity increases to 33.3% in Caucasians.

The human CDC25C gene maps to chromosome 5q31, a site of frequent loss of heterozygosity

Sartor *et al.* (2) mapped the human CDC25 gene to 5q31 by fluorescence in situ hybridization using the cDNA cloned by Sadhu *et al.* This mapping location was confirmed by Taviaux and Demaille (3), also using fluorescence in situ hybridization. There have been many studies of LOH on 5q, particularly the 5q21-

q22 region where the Adenomatous Polyposis Coli (APC) tumor suppressor gene lies. The most extensively studied cancers are those of the gastrointestinal tract, lung and ovary. There have been fewer studies of the 5q23-q33 region just distal to APC (where CDC25C lies), however the available data suggests that LOH occurs in this region at a frequency of ~30% in cervical cancer (4), 20-40% in colon cancer (5,6), 30-50% in ovarian cancer (7,8), up to 38% in stomach cancer (9), and 23% in testicular cancer (10). There is also evidence for LOH in head and neck, lung and liver cancers. In most of these studies only one or two markers were used. Definitive assessment of LOH frequency at the CDC25C locus will require direct analysis of the polymorphisms identified in various tumor types.

References

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Example 43. Dihydropyrimidine Dehydrogenase (DPD)

DPD is conditionally essential

Dihydropyrimidine Dehydrogenase is essential for cell survival in the presence of pyrimidine nucleotide analogs such as 5-FU and fluorodeoxyuridine. 5-fluorouracil (5-FU) and related compounds are antineoplastic drugs used in the treatment of breast, gastrointestinal, head and neck and other cancers. These drugs have widely varying clinical effects in cancer patients, ranging from induction of complete response (tumor disappearance) in some patients to severe toxicity in others. There is currently no reliable basis for predicting individual patient responses, and therefore patients receiving 5-FU must be monitored carefully for toxic reactions.

There are a variety of anabolic and catabolic pathways that affect the action of 5-FU (reviewed in Goodman and Gilman, *The Pharmacological Basis of Therapeutics*, 8th edition). For example, in order to exert its antiproliferative effects the pyrimidine analog 5-FU must be converted enzymatically to the nucleotide level (fluorodeoxyuridine) by phosphorylation and ribosylation; fluorodeoxyuridine is sometimes given directly because it bypasses most of these steps, and simply requires phosphorylation by thymidine kinase. The 5-fluoronucleotide is an irreversible inhibitor of thymidylate synthase, the enzyme which converts dUMP to dTMP and is required for de novo synthesis of thymidine, and hence for DNA

synthesis.

There is a three step pathway for catabolism of pyrimidines (thymine and uracil) to beta alanine. Pyrimidine analogs such as 5-FU are catabolized by the same pathway. The first and rate limiting step in this pathway is catalyzed by dihydropyrimidine dehydrogenase (DPD). DPD accounts for catabolism of as much as 90% of a 5-FU dose in normal individuals, and the half life of 5-FU in normals is ~8-20 minutes. Patients homozygous for mutant DPD alleles have been identified, a condition variously called DPD Deficiency, Hereditary Thymine-Uraciluria or Familial Pyrimidinemia. In such patients ~90% of 5-FU is excreted unchanged in the urine, and the drug has a half life longer than 2.5 hours. As a result of the drastically reduced catabolism of 5-FU the toxic effects of the drug are magnified and patients are subject to severe toxic reactions. There are reports of deaths in patients with DPD deficiency after treatment with 5-FU. Thus cell (and organism) survival in the presence of 5-FU depends on presence of functional DPD protein to transform 5-FU to the inactive dihydroxy metabolite.

This principal has also been demonstrated in cancer cells both in vitro and in vivo: cancer cells with lower DPD levels are more susceptible to the toxic effects of 5-FU. It has been suggested that measuring DPD levels would be useful for calibration of 5-FU dosage.

The DPD gene exhibits variances

We have identified four common sites of variance in DPD mRNA by screening cDNA from 36 unrelated individuals. The variant nucleotides are 166, 577, 3925 and 3937 (see DPD Variance Table; numbering is from Yokota, et al. cDNA Cloning and Chromosome Mapping of Human Dihydropyrimidine Dehydrogenase, an Enzyme Associated with 5-fluorouracil Toxicity and Congenital Thymine

Uraciluria. Journal of Biological Chemistry. 269: 23192-23196, 1994). Two of the variances in nucleotide sequence alter the amino acid coding sequence: amino acid 29 is usually cysteine but arginine alleles were also detected; cys/arg heterozygotes were found at a frequency of 11%. Residue 166 of DPD is reported to be methionine but valine is present at 166 in some alleles; 9% of the population surveyed are met/val heterozygotes. One double heterozygote was identified out of 36 patients. Both these amino acid polymorphisms are located in the N-terminal NAD/FAD binding domain of DPD. Residue 166 is located in a highly conserved domain of DPD. Two other polymorphisms are located in the 3' untranslated region of DPD, only 11 nucleotides apart.

The DPD gene maps to chromosome 1p22, a region frequently subject to LOH in different cancers

The DPD gene has been mapped to chromosome 1p22 by fluorescence in situ hybridization. LOH at 1p22 has been reported in colon, breast, and other cancers.

Allele specific inhibition of DPD to potentiate 5-FU action in cancer cells with LOH at the DPD locus

The DPD gene is polymorphic and conditionally essential in the presence of 5-FU. These properties can be exploited in a therapeutic strategy for cancer patients with LOH at the DPD locus. Specifically, in a patient with two alternative alleles for DPD in normal cells and one allele in cancer cells due to LOH, an allele specific drug can be used to sensitize cancer cells to the action of 5-FU by inhibiting its catabolism. Cancer cells (but not normal cells) would be poisoned by high levels of 5-FU due to low clearance. Normal cells, containing an uninhibited allele, would be able to catabolize DPD at close to normal levels.

Alternatively, patients heterozygous for functional and defective copies of DPD,

and in whom LOH resulted in loss of the functional allele, could be treated by 5-FU without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at DPD and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to 5-FU even though they might have cancers not traditionally treated with pyrimidine analogs.

Example 44. Fanconi Anemia genes A, B, C, D, E, F, G and H (FAA, FAB, FAC, FAD, FAE, FAF, FAG, FAH)

The Fanconi Anemia genes are conditionally essential.

The Fanconi Anemia genes are essential for cell growth or survival in the presence of DNA cross linking agents. In order for cells to survive or proliferate in an abnormal environment characterized by the presence of DNA cross linking molecules such as Mitomycin C and diepoxybutane it is necessary that the cells are capable of efficiently repairing damage caused by these agents. Cells contain proteins necessary for such repair. One way such repair proteins can be identified is by absence of function in specific patients who, as a consequence, are particularly susceptible to the toxic effects of cross linking agents.

Fanconi Anemia (FA) is a hereditary disease, autosomal recessive in transmission, characterized by progressive bone marrow failure, birth defects and predisposition to malignancies. FA patients are hypersensitive to the toxicity of DNA cross linking agents. This hypersensitivity can be measured in cultured FA cells, which is one method used to establish the diagnosis of FA.

Patients heterozygous for defective FA genes are generally not hypersensitive to

DNA crosslinking agents in contrast to those that are homozygous. This suggests that treating heterozygous cancer patients with an inhibitor specific for one allele of the FA gene (and thereby reducing levels of FA protein function by up to 50% in normal cells) would be well tolerated. Inhibition of the FA allele present in cancer cells but not the alternative form present only in normal cells would make cancer cells selectively sensitive to crosslinking agents, leading to a cytotoxic antiproliferative effect. Normal cells would be able to repair damage caused by such agents, by analogy to the clinical data from patients heterozygous for defective FA genes.

The FA genes and gene products are polymorphic

Seven FA genes have been identified by complementation studies. The genes for FAA and FAC have been cloned. DNA variances have been reported in both genes. For example, Savino et al. report three variances in FAA, all of which alter the protein coding sequence. (Savino, M., et al. Mutations in the Fanconi Anemia Group A Gene (FAA) in Italian Patients. American Journal of Human Genetics 61:1246-1253, 1997.) The location of these variances is shown in the Table below, reproduced from the paper by Savino.

Variances in the FAA Gene

Polymorphic nucleotide	Alternate bases	Affected amino acid residue	Alternate amino acids	Frequency of rare allele
796	A, G	266	Thr, Ala	.29
1501	G, A	501	Gly, Ser	.40
2426	G, A	809	Gly, Asp	.30

FA genes map to chromosomes that are frequently subject to LOH in different cancers

The FAC gene maps to chromosome 9q22.3, (as do three other FA complementation

groups according to Stratthdee, C.A., et al. Evidence for at least four Fanconi anaemia genes including FACC on chromosome 9. *Nature Genetics* 1: 196-198, 1992). The FAA gene maps to chromosome 16q24.3. FAD maps to 3p26-p22. All FA genes mapped so far lie in regions subject to frequent LOH. LOH affecting chromosome 9 is well documented in many cancers. For example, loss of the 9q arm is well documented in cancers such as bladder, esophagus, ovary, testis and uterus. LOH frequencies in these cancers range from 20% to 62%. LOH affecting chromosome arm 16q, particularly the 16q24 region is well documented, particularly in breast, prostate and liver cancers. For example, in six detailed studies of breast cancer in the 16q22-q24 region LOH frequencies of 40-60% have been reported. Further, 16q22 LOH has been reported in 25-90% of liver cancers, with the average around 45%. Less extensive studies of other cancer types report 16q22 LOH in 19% of bladder cancers, 20% of colon cancers, 19-27% of esophageal cancers, 25% of small cell lung cancers, 16-37% of ovarian cancers 22% of uterine cancers, and 31-50% of prostate cancers. Loss of chromosome 3p26-21 is common in lung cancer, kidney cancer, head and neck cancer and breast cancer among other cancers. Reports of >50% LOH are common in these cancer types.

Other genes conditionally essential for response to DNA cross linking agents

In a related aspect, other genes which, when defective, sensitize cells to toxic effects of DNA crosslinking agents would be amenable to the therapeutic strategy outlined above for the FA genes. Specifically, in a patient with two alternative alleles for such a gene and LOH at the relevant locus, an allele specific drug could be used to sensitize cancer cells to the action of cross linking agents. Such drugs could then be used to treat cancer patients constitutionally heterozygous for two normal alleles at the relevant locus, in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist in the administration of the appropriate allele specific inhibitor plus a cross linking agent or treatment to induce damage in all cells. Cancer

cells (but not normal cells) would be rendered unable to respond by inhibition of expression of the relevant repair gene. Examples of such genes are the excision repair cross complementing (ERCC) genes, twelve of which have been identified (see Target Gene Table). Defects in these genes are associated with Xeroderma Pigmentosum and Cockayne Syndrome. (Scriver, C. R. et al., The Metabolic and Molecular Bases of Inherited Disease, 7th edition, McGraw Hill, New York, 1995.)

Alternatively, patients heterozygous for functional and defective copies of such genes, and in whom LOH resulted in loss of the functional allele, could be treated by a cross-link inducing procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to cross linking agents or procedures even though they might have cancers not traditionally treated with such agents.

Example 45. Asparagine Synthetase (AS).

Variagenics Target Gene _____

Asparagine Synthase is conditionally essential

Cells require a continuous supply of amino acids for protein biosynthesis. Cells can import amino acids from serum via amino acid transporters (the only source besides protein catabolism for the ten essential amino acids), or amino acids cells can be synthesized *de novo* by cells (only an option for the ten nonessential amino acids). The essential amino acids are isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, valine and histidine. Alterations in the nutritional environment of growing cells that result in a decreased extracellular concentration of essential amino

acids cause arrested cell growth and may result in cell death.

Even a nonessential amino acid can become essential in a cell where (i) at least one enzyme required for its biosynthesis is not expressed (perhaps due to downregulation in response to an abundant extracellular supply of the amino acid), or (ii) the biosynthetic pathway is blocked by an inhibitor.

Asparagine is a nonessential amino acid which is, however, essential for survival of rapidly dividing cells that are not expressing asparagine synthetase, the terminal enzyme in asparagine biosynthesis. Asparagine synthetase, considered to be a housekeeping gene, catalyzes the ATP dependent conversion of aspartic acid to asparagine in mammalian cells. A number of different cancer types do not usually express asparagine synthetase, including childhood acute leukemias. One common therapeutic used in the treatment of childhood acute lymphocytic leukemia is the enzyme L-asparaginase (purified from *E. coli* or *Erwinia carotovora*) which, upon injection, rapidly depletes serum asparagine (by hydrolysis to aspartate), thereby lowering blood levels of asparagine to undetectable levels within hours of injection. (Ohnuma, T. et al. Biochemical and Pharmacological Studies with L-Asparaginase in Man. Cancer Research 30: 2297-2305, 1970.) Leukemic cells have high rates of protein synthesis but do not express asparagine synthetase and are therefore highly vulnerable to the rapid loss of asparagine and consequent shutdown of protein synthesis. Cell death after L-asparaginase induced asparagine starvation has been shown to be apoptotic. (Bussolati, O. Characterization of Apoptotic Phenomena Induced by Treatment with L-Asparaginase in NIH3T3 Cells. Experimental Cell Research 220: 283-291, 1995.) After one or more doses leukemic cells often become resistant to L-asparaginase due to induction of asparagine synthetase activity and consequent autonomy for asparagine.

In a patient with two alternative alleles for asparagine synthetase and LOH at 7q, an

allele specific drug could be used to sensitize cancer cells to the action of L-asparaginase. Such drugs could then be used to treat cancer patients constitutionally heterozygous for two normal alleles at the asparagine synthetase locus, in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist in the administration of the appropriate allele specific inhibitor plus L-asparaginase to deplete the concentration of this amino acid in serum while rendering cancer cells (but not normal cells) unable to respond by upregulating asparagine synthetase.

The Asparagine Synthetase gene maps to chromosome 7q21.3, a region frequently subject to LOH in different cancers

The asparagine synthetase gene has been mapped to chromosome 7q21.3 by fluorescence in situ hybridization, following localization to 7q by analysis of somatic cell hybrids. The q21 region of chromosome 7 is subject to frequent LOH, particularly in colon, breast and prostate cancers. 7q21.3 LOH is detected in up to 50% of colon cancers, up to 37% of prostate cancers (83% of prostate cancers have LOH in the adjacent chromosome band, 7q31) and in 10-55% of breast cancers, where again, there is even more frequent LOH in 7q31. LOH at 7q21 has also been reported in uterine cancer and head and neck cancer. Several other cancer types have not yet been well studied for LOH affecting this region.

Example 46. Methionine Synthase (MS).

Variagenics Target Gene _____

Methionine Synthase is conditionally essential in dividing cells

Cells require a continuous supply of amino acids for protein biosynthesis. L-

methionine is one of ten essential amino acids. Consequently dividing cells must obtain their methionine from serum via amino acid transporter (the only source besides protein catabolism for the ten essential amino acids). Alterations in the nutritional environment of growing cells that result in a decreased extracellular concentration of essential amino acids such as methionine cause arrested cell growth and may result in cell death. Cancer cells are particularly sensitive to methionine deprivation. (Tan, Y., et al., Anticancer Efficacy of Methioninase in vivo. *Anticancer Research* 16: 3931-3936.)

The cellular requirement for methionine can be bypassed: if L-homocysteine is provided to cells it can be methylated to form methionine by the enzyme methionine synthase (MS). In this reaction the methyl group is provided by 5-methyltetrahydrofolate and MS-bound methylcobalamin serves as an intermediate methyl carrier. A second enzyme may be required for reductive activation of methionine synthase, based on complementation studies.

It occurred to the inventors that the apparent antineoplastic effects of methionine deprivation could be enhanced and made tumor cell specific by preventing cells from converting endogenous homocysteine to methionine by allele specific inhibition of methionine synthase (or other enzymes required for the conversion of homocysteine to methionine; see: Scriver, C., et al., editors, The Metabolic and Molecular Basis of Inherited Disease. McGraw Hill, New York, pp. 3111-3128 and 3129-3149). This strategy would be useful in cancer patients that are heterozygous for methionine synthase (or another enzyme required for conversion of homocysteine to methionine) and who have LOH at the methionine synthase (or other) gene locus. In such patients an allele specific inhibitor of MS directed to the sole allele present in cancer cells, coupled with methionine starvation or methioninase treatment, would selectively prevent tumor cells from responding to methionine deprivation. The provision of supplemental homocysteine, which could only be converted to methionine by the

normal cells, would provide a way to amplify the differential toxicity to cancer cells. Also, the methionine analog ethionine has been shown to potentiate the effects of methionine starvation. (Poirson-Bichat, F., et al., Growth of methionine-dependent human prostate cancer (PC-3) is inhibited by ethionine combined with methionine starvation. Br. J. Cancer 75: 1605-1612.) Ethionine or similar agents could be used
5 in conjunction with an allele specific inhibitor of methionine synthesis.

An alternative approach to allele specific therapy of cancer cells with LOH would be to target the amino acid transport system for methionine in patients heterozygous for
10 this protein and in whom only one allele is present in cancer tissue as a result of LOH. This would result in selective methionine starvation for cancer cells. Allele specific transport inhibition could be combined with methionine starvation or methioninase treatment to enhance the cytotoxic effect.

15 *The Methionine Synthase gene maps to chromosome 1q43, a region subject to LOH in several cancers*

The MS gene has been mapped to chromosome 1q43 by fluorescence in situ hybridization. The q43 region of chromosome 1 is subject to frequent LOH
20 particularly in colon, head and neck, ovarian and liver cancers, where LOH frequencies vary from 11 to 39%. LOH at 1q43 has also been reported in cervix, pancreas, stomach and testis cancers. Several other cancer types have not yet been well studied for LOH in this region.

25 *Other amino acid biosynthetic enzymes are candidates for allele specific inhibition*

It will be evident to one skilled in the art that strategies similar to those described above for asparagine (an essential amino acid) and methionine (a non-essential amino acid) could be undertaken for other amino acid biosynthetic enzymes. For example,

L-glutaminase has also been shown to have antiproliferative effects on mammalian cell growth. Allele specific blockade of glutamine synthesis in heterozygous patients with LOH for genes essential for glutamine synthesis could be the basis of a cancer specific therapy.

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Example 47. Methylthioadenosine phosphorylase (MTAP).

Variagenics Target Gene _____

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Methylthioadenosine phosphorylase can convert methylthioadenosine to methionine, an essential amino acid

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Cells require a continuous supply of amino acids for protein biosynthesis. L-methionine is one of ten essential amino acids. Consequently dividing cells must obtain methionine from serum via amino acid transporter (the only source besides protein catabolism or conversion of L-homocysteine). Alterations in the nutritional environment of growing cells that result in a decreased extracellular concentration of essential amino acids such as methionine cause arrested cell growth and may result in cell death. Cancer cells are particularly sensitive to methionine deprivation. (Tan, Y., et al., Anticancer Efficacy of Methioninase in vivo. *Anticancer Research* 16: 3931-3936.)

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The cellular requirement for methionine can be bypassed by conversion of L-homocysteine to methionine as discussed above. An alternative pathway for methionine synthesis is conversion of 5'-methylthioadenosine (5'-MTA) via the action of 5'-MTA phosphorylase (MTAP). (Tisdale, M.J., Methionine Synthesis from 5'-methylthioadenosine by Tumor Cells. *Biochemical Pharmacology* 32: 2915-2920.) In tissue culture experiments low concentrations of 5'-MTA can substitute for

methionine in some cell lines. Thus 5'-MTA can rescue cells from methionine deprivation.

5 It occurred to the inventors that allele specific inhibition of MTAP in cancer patients heterozygous for MTAP and whose cancer cells have only one allele of MTAP as a consequence of LOH, in combination with methionine deprivation (methionine starvation or L-methioninase treatment) and dietary supplementation with 5'-methylthioadenosine would provide a source of convertible methionine substrate selectively useful to normal cells. Tumor cells would have no source of methionine,
10 being unable to convert the 5'-methylthioadenosine, and hence would be selectively poisoned. This therapeutic strategy would not necessarily require an allele specific inhibitor as *all copies* of MTAP are deleted in some cancers. Such cancers should be differentially poisoned vis a vis normal cells by methionine deprivation in the presence of 5'-methylthioadenosine.

15 *The MTAP gene maps to 9p21, a region frequently subject to LOH in many cancers*

The MTAP gene has been mapped to chromosome 9p21 by physical techniques (pulsed field gel electrophoresis and yeast artificial chromosome mapping). The gene
20 lies near the cyclin dependent kinase inhibitors p16 and p15 which are frequently reduced to one or zero copies in cancer cells. (Nobori, et al., Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers. *Proc. Natl. Acad. Sci. U.S.A.* 93: 6203-6208.) The p21 region of chromosome 9 is subject to frequent LOH particularly in cancers of the bladder, breast,
25 esophagus, head and neck, kidney, lung, melanoma and ovary. The frequency of LOH in these cancers ranges from 20% to nearly 100%.

Example 48. DNA dependent protein kinase (DNA-PK) and associated factors.
Variagenics Target Genes _____

DNA dependent protein kinase is conditionally essential

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Cells exposed to ionizing radiation, such as gamma radiation, are damaged by base modifications and DNA strand breaks. Double strand DNA breaks are among the most lethal form of radiation damage; one such break, if unrepaired, can be cell lethal. Four complementation groups of mammalian cell mutants that are defective in repair of double strand (ds) breaks have been identified. All four complementation groups are hypersensitive to ionizing radiation. The loci for three of these groups have been shown to encode components of DNA-dependent protein kinase (DNA-PK). The fourth group is deficient in the gene encoding XRCC4, a factor that associates with and stimulates DNA Ligase IV. Ligation of ds breaks by DNA ligase IV in a cell free system is increased 7-8 fold by co-expression of XRCC4.

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DNA-PK is a multiprotein complex with a DNA binding regulatory subunit, the Ku heterodimer [Ku70 (XRCC6) and Ku80, also referred to as Ku86 (XRCC5)], and a catalytic subunit, DNA-PKcs (probably XRCC7), that is activated by the regulatory subunit upon binding to DNA ds ends, with consequent expression of serine/threonine kinase activity resulting in phosphorylation of a variety of DNA binding proteins. A fourth protein called KARP-1 is expressed from the Ku80/86 locus and is also implicated in DNA-PK function.

20

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Cells lacking any of the components of DNA-PK are exquisitely sensitive to gamma irradiation. This has been demonstrated directly in mice with targeted disruption of the Ku80/86 and DNA-PKcs genes. The Ku80/86 deficient mice were also sensitive to methyl methane sulfonate, a DNA alkylating agent that induces single strand breaks and to etoposide, a topoisomerase II inhibitor. Thus the components of DNA-PK can

also be important for repair of a variety of chemically induced DNA lesions as well as ionizing radiation.

5 In a cancer patient with two alternative alleles for a component of DNA-PK and LOH at the heterozygous locus, an allele specific inhibitory drug could be used to sensitize cancer cells to the action of ds break inducing treatments. Such a drug could be used to treat cancer patients constitutionally heterozygous for two normal alleles at any of the DNA-PK loci in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist in the administration of the appropriate allele specific inhibitor plus a ds break inducing agent or procedure. The tumor cells would be unable to effectively repair ds breaks, while the uninhibited allele in normal cells would be able to function. Alternatively, patients heterozygous for functional and defective copies of genes required for repair of strand breaks, and in whom LOH resulted in loss of the functional allele, could be treated by a strand break inducing procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to strand breaking agents or procedures (exposure to ionizing radiation) even though they might have cancers not traditionally treated with such measures.

The genes encoding constituents of DNA-PK map to chromosomes frequently subject to LOH in different cancers

25 The DNA-PKcs gene has been mapped to 8q11, the Ku80/86 gene to 2q11-q13 and the Ku70 gene to 22q11-q13. All three regions are subject to LOH in different cancers. LOH on 2q has been reported in lung ovary and cervical cancers at frequencies ranging from 11% to 39%. LOH for 8q has been reported in cervix, head and neck, kidney, lung, ovary, prostate and testis cancers at frequencies ranging from 20% to 50% of

cancers. LOH on 22q has been reported in brain, breast colon, head and neck, lung, ovary, pediatric and stomach cancers at frequencies ranging from 10 to 76%. Several other cancer types have not yet been well studied for LOH affecting either region.

5 *Other proteins required for repair of DNA strand breaks are also candidates for allele specific therapy of cancer*

10 It will be evident to one skilled in the art that strategies similar to those described above for DNA-PK could be undertaken for other proteins required for repair of DNA strand breaks. For a recent review of such proteins see: Zdzienicka, M.Z., Mammalian mutants defective in the response to ionizing radiation-induced DNA damage. *Mutation Research* 336: 203-213, 1995; Thompson, L.H. and P.A. Jeggo, Nomenclature of human genes involved in ionizing radiation sensitivity. *Mutation Research* 337: 131-134, 1995; Thacker, J. and R.E. Wilkinson, The genetic basis of cellular recovery from radiation damage: response of the radiosensitive irs lines to low-dose rate irradiation. *Radiation Research* 144: 294-300, 1995. Two other syndromes with hypersensitivity to X-rays are Diamond-Blackfan anemia and aplastic anemia (Diemen, P.C., X-ray-sensitivity of lymphocytes of aplastic- and Diamond-Blackfan-anemia patients as detected by conventional cytogenetic and chromosome painting techniques. *Mutation Research* 373: 225-235, 1997). Recently evidence of several other genes responsible for DNA double strand break repair has been described. (Nicolas, N., Finnie, N.J., et al., *Eur. J. Immunol.* 26:1118-1122, 1996.) The above genes which, when defective, sensitize cells to toxic effects of DNA strand breaking agents would be amenable to the therapeutic strategy outlined above for the DNA-PK genes. Specifically, in a patient with two alternative alleles for such a gene and LOH at the relevant locus, an allele specific drug could be used to sensitize cancer cells to the action of strand breaking agents. Such drugs could then be used to treat cancer patients constitutionally heterozygous for two normal alleles at the relevant locus, in whom LOH had rendered cancer cells hemizygous or homozygous for one allele.

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Treatment would consist in the administration of the appropriate allele specific inhibitor plus a strand breaking agent or treatment to induce damage in all cells. Cancer cells (but not normal cells) would be rendered unable to respond by inhibition of expression of the relevant repair gene.

5

Alternatively, patients heterozygous for functional and defective copies of genes required for repair of strand breaks, and in whom LOH resulted in loss of the functional allele, could be treated by a strand break inducing procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to strand breaking agents or procedures (exposure to ionizing radiation) even though they might have cancers not traditionally treated with such measures.

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Example 49. Ataxia Telangiectasia Mutated (ATM) and c-Abl
Variagenics Target Gene _____

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The Ataxia Telangiectasia gene is essential for cell growth or survival in the presence of ionizing radiation or DNA damaging molecules

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In order for cells to survive or proliferate in the presence of ionizing radiation (IR) or radiomimetic chemicals it is necessary that they are capable of efficiently repairing IR induced damage. Cells contain proteins necessary for such repair. One way such proteins can be identified is by their absence in specific patients who are particularly susceptible to the toxic effects of IR.

Ataxia Telangiectasia (AT) is a genetically transmitted autosomal recessive disorder characterized by variable degrees of immunodeficiency, telangiectasia (small blood vessels growing near the surface of the skin or eye), cerebellar ataxia (loss of balance due to abnormal development of the cerebellum) and increased sensitivity to both ionizing radiation and radiomimetic drugs, including bleomycin; AT cells are killed by lower doses of ionizing radiation or radiomimetic drugs than normal cells. Further, heterozygotes for mutant and normal AT alleles have radiation sensitivity close to that of homozygous normals. Therefore cancer cells from individuals heterozygous for null alleles of the AT gene (called ATM) should be highly susceptible to radiation therapy when only the deficient AT allele remains in cancer cells due to LOH, compared to normal cells from the same patients. Such patients could be treated by a DNA damage inducing procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to strand breaking agents or procedures (such as exposure to ionizing radiation) even though they might have cancers not traditionally treated with such measures. In a related aspect, this approach is applicable to heterozygotes for other genes associated with ATM-mediated radiosensitivity. One such protein is the c-Abl protein tyrosine kinase, which binds to the ATM protein and regulates its function. c-Abl is known to be important in the stress response to ionizing radiation. One of its functions is activation of stress activated protein kinases (SAPKs) after irradiation or exposure to alkylating agents such as *cis*-platinum or mitomycin C, a response that is defective in ATM cells. Correction of the SAPK activation defect in ATM cells by non-mutant ATM cDNA suggests that the ATM - c-Abl interaction is necessary for the DNA damage response. (Kharbanda, S., et al. *Nature* 376: 785-788, 1995.)

In a cancer patient with two alternative functional alleles for a component of ATM and LOH at the ATM locus, an allele specific inhibitory drug could be used to sensitize

cancer cells to the action of DNA damage inducing treatments such as ionizing radiation or radiomimetic drugs. Such an allele specific drug could be used to treat cancer patients constitutionally heterozygous for two normal ATM alleles in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist of the administration of the appropriate allele specific inhibitor plus a DNA damage inducing treatment or procedure. The tumor cells would be unable to effectively the DNA damage, while the uninhibited allele in normal cells would be able to function. A similar approach could be taken to

The ATM gene is polymorphic

The ATM cDNA is 9.58 kb. Several likely polymorphisms have been identified, although population studies have not yet been performed to determine allele frequencies. One of the reported polymorphisms, an ATG to ATA change in codon 847, results in a methionine vs. isoleucine difference. Thus ATM is potentially targetable at the DNA, RNA and protein levels. It is likely that additional variances will be identified with broader population surveys and computational variance detection.

The ATM gene maps to chromosome 11q23 and the c-Abl gene maps to 9q34.1, two regions of high frequency LOH in different cancer types

Chromosome 9q34 is lost in a high fraction of bladder, esophagus, ovary, head & neck and testis cancers (17 - 76%) and in a lesser fraction of breast, liver and prostate cancers and leukemias. Chromosome 11q23 is lost in brain, cervix, esophagus, breast, kidney, colon, stomach, head & neck and lung cancers at frequencies ranging from 16% to 100%.

Other proteins required for repair of DNA damage are also candidates for allele specific therapy of cancer

It will be evident to one skilled in the art that strategies similar to those described above for ATM and c-Abl could be undertaken for other proteins required for the stress response to DNA damaging agents, such as other stress activated protein kinases or downstream effector proteins.

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Methylguanine Methyltransferase (MGMT)**Gene VARIA 1534**

The methylguanine methyltransferase gene is essential for cell growth or survival in the presence of alkylating agents

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Methylguanine methyltransferase (MGMT) is a suicide protein that repairs alkylating agent damage, specifically alkylation of the ⁶O position of guanine. Alkyl groups are covalently bound to an active site cysteine (residue 145) of MGMT, thereby irreversibly inactivating the protein. ⁶O-benzylguanine is an analog inhibitor of MGMT that, by inactivating MGMT, renders tumor cells more sensitive to the toxic effects of methylating and chloroethylating agents. MGMT is thus a conditionally essential gene in the presence of such drugs. ⁶O-benzylguanine is being developed as a chemosensitizing agent.

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In a cancer patient with two alternative functional MGMT alleles an allele specific inhibitory drug could be used to sensitize cancer cells to the action of alkylating agents. Such an allele specific drug could be used to treat cancer patients constitutionally heterozygous for two normal MGMT alleles in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist of the administration of the appropriate allele specific inhibitor plus an alkylating agent. The tumor cells would be unable to effectively repair the alkylating agent induced DNA damage, while the uninhibited allele in normal cells would be able to function.

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The MGMT gene is polymorphic

Several variances have been reported in human MGMT, or discovered by Variagenics, including three protein polymorphisms. There is a silent C/T variance at position 255 (11% heterozygotes among 36 individuals surveyed), another C/T variance at nt. 346

which results in a L84F amino acid variance (5% heterozygotes), an A/G variance at nt. 523 which results in a I143V amino acid variance (24% heterozygotes). A variance has been reported in Japanese at codon 160, GGA vs. AGA, converting glycine to arginine. 15% of the population studied were heterozygotes.

5

The alteration of glycine 160 to arginine reduced the inactivation by O6-benzylguanine with an approximately 20 fold increase in the IC50 concentration. These results demonstrate variance-specific effects of a small molecule, O6-benzylguanine, on normal (non-mutant) alleles of the conditionally essential MGMT gene.

10

Administration of O6 benzylguanine to patients who are heterozygous for the residue 160 gly/arg variance in their normal cells, and contain only the form of the gene with a glycine residue at position 160 in their cancer cells, together with methylating or chloroethylating agents for chemotherapy, will be specifically toxic to cancer cells without increasing toxicity to normal cells.

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References

1. Imai, Y, *Carcinogenesis* (1995), 16:2441-24445
2. Edara, S. (1996) Resistance of the human O6-alkylguanine-DNA alkyltransferase containing arginine at codon 160 to inactivation by O6-benzylguanine. *Cancer Research* 56, 5571-5575.

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All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

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One skilled in the art would readily appreciate that the present invention is well

adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The groups of genes and the particular genes described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. For example, those skilled in the art will readily recognize that the methods and inhibitors can utilize a variety of different target genes within the groups described. Thus, such additional embodiments are within the scope of the present invention and the following claims.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

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In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

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Thus, additional embodiments are within the scope of the invention and within the following claims.

CLAIMS

What we claim is:

5 1. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

 (a) determining at least two alleles of a said gene, wherein said gene
10 encodes a product required for cell proliferation;

 (b) testing a potential allele specific inhibitor to determine whether said
 potential allele specific inhibitor is active on at least one but less than all of said alleles;
 wherein inhibition of expression of at least one but less than all of said alleles
 or reduction of the level of activity of a product of at least one but less than all of said
15 alleles in the presence of said potential allele specific inhibitor is indicative that said
 potential allele specific inhibitor is a said inhibitor.

2. A method for identifying an inhibitor potentially useful for treatment of
cancer, wherein said inhibitor is active on a gene vital for cell growth or viability,
20 and wherein said gene is subject to loss of heterozygosity in a cancer, said method
 comprising the steps of:

 (a) determining at least two alleles of a said gene, wherein said gene
 encodes a product required to maintain inorganic ions and vitamins at levels
 compatible with cell growth or survival;

25 (b) testing a potential allele specific inhibitor to determine whether said
 potential allele specific inhibitor is active on at least one but less than all of said
 alleles;

 wherein inhibition of expression of at least one but less than all of said alleles
 or reduction of the level of activity of a product of at least one but less than all of

said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

5 3. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

10 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

15 wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

20 4. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

25 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

 wherein inhibition of expression of at least one but less than all of said alleles

or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

5 5. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

10 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

15 wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

20 6. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

25 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

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wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

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7. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

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(a) determining at least two alleles of a said gene, wherein said gene is located on a high frequency LOH chromosomal region;

(b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

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wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

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8. The method of claim 7, wherein said gene is located on a chromosomal arm which has a frequency of allele loss of at least 15% in a cancer.

9. The method of claim 7, wherein said gene is located in proximity to a chromosomal marker which undergoes LOH at a frequency of at least 10% in a cancer.

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10. The method of claim 7, wherein said gene is located in proximity to a tumor suppressor gene which undergoes LOH at a frequency of at least 10% in a cancer.

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11. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

5 (a) determining at least two alleles of a said gene, wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene;

(b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

10 wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

15 12. The method of claim 11, wherein said gene is located on a high frequency LOH chromosomal region.

20 13. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required for cell proliferation, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

25 14. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, said gene has at least two alternative

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alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

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15. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain organic compounds at levels
10 compatible with cell growth or survival, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

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16. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain cellular proteins at levels
compatible with cell growth or survival, said gene has at least two alternative alleles in a population, and

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wherein said inhibitor targets at least one but less than all of said alternative alleles.

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17. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain cellular nucleotides at levels
compatible with cell growth or survival, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

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18. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

19. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene is located on a high frequency LOH chromosomal arm region, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

20. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

21. A pharmaceutical composition, comprising

at least one allele specific inhibitor targeting at least one but less than all allelic forms of an essential gene in a population, wherein said gene encodes a product required for cell proliferation; and

a pharmaceutically acceptable carrier or excipient.

22. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain inorganic ions and vitamins at levels compatible with
cell growth or survival; and
a pharmaceutically acceptable carrier or excipient.

23. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain organic compounds at levels compatible with cell
growth or survival; and
a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain cellular proteins at levels compatible with cell growth
or survival; and
a pharmaceutically acceptable carrier or excipient.

25. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain cellular nucleotides at levels compatible with cell
growth or survival; and
a pharmaceutically acceptable carrier or excipient.

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26. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain the integrity and function of cellular and subcellular
structures; and

a pharmaceutically acceptable carrier or excipient.

27. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene is located on a
high frequency LOH chromosomal arm region; and

a pharmaceutically acceptable carrier or excipient.

28. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene has at least two
sequence variances which occur at frequencies such that at least 10% of a population
is heterozygous for said gene; and

a pharmaceutically acceptable carrier or excipient.

29. A method for producing an inhibitor potentially useful for cancer treatment,
wherein said inhibitor is active on at least one but less than all alternative alleles of
a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative
allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is
deleted in a cancer cell, and wherein said gene encodes a product required for cell
proliferation;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

30. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

31. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

32. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

33. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival;

(b) screening to identify an inhibitor which inhibits said at least one but less

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than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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34. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

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(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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35. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

25

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene is located on a high frequency LOH chromosomal arm region;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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36. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

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(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

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(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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37. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required for cell proliferation; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

38. The method of claim 37, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

39. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

40. The method of claim 39, wherein the cells of said precancerous condition are

not clonal from a single cell, further comprising the step of:

5 b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

10 41. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

15 a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival; and
20 wherein cells of said precancerous condition have undergone LOH of said first gene.

42. The method of claim 41, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

25 b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in

cells of said precancerous condition.

43. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

5 a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form
10 present in said normal somatic cells, and said first gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival; and
wherein cells of said precancerous condition have undergone LOH of said first gene.

15 44. The method of claim 43, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific
20 inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

25 45. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are

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heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival; and

5 wherein cells of said precancerous condition have undergone LOH of said first gene.

46. The method of claim 45, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

10 b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for
15 each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

47. A method for preventing the development of cancer in a patient having a
20 precancerous condition, comprising the steps of:

 a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than
25 all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain the integrity and function of cellular and subcellular structures; and

 wherein cells of said precancerous condition have undergone LOH of said first gene.

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48. The method of claim 47, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

49. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene is located on a high frequency LOH chromosomal arm region; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

50. The method of claim 49, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for

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each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

51. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

52. The method of claim 51, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

53. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of: administering a therapeutic amount of an allele specific inhibitor active on at

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least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required for cell proliferation, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

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54. The method of claim 53, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

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(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

55. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

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administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

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56. The method of claim 55, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

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(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

57. A method for treating a patient suffering from a cancer, wherein said patient

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is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

58. The method of claim 57, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

59. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

60. The method of claim 59, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

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(c) both (a) and (b).

61. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

5 administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic
10 form of said gene is present in cancer cells in said patient.

62. The method of claim 61, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

15 (b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

63. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

20 administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic
25 form of said gene is present in cancer cells in said patient.

64. The method of claim 63, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are

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heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

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65. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

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wherein said gene is located on a high frequency LOH chromosomal arm region, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

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66. The method of claim 65, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

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(c) both (a) and (b).

67. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

25

wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said

patient.

68. The method of claim 67, further comprising the steps of:

5 (a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

10 69. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene encodes a product required for cell proliferation, and wherein said inhibitor is less active on at least one other allele of said gene.

15 70. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

20 wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, and wherein said inhibitor is less active on at least one other allele of said gene.

71. A method of inhibiting growth of a cell comprising the step of:

25 administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival, and wherein said inhibitor is less active on at least one other allele of said gene.

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72. A method of inhibiting growth of a cell comprising the step of:
administering at least one inhibitor active on an allele of a gene vital for cell
viability or growth,

wherein said gene encodes a product required to maintain cellular proteins
at levels compatible with cell growth or survival, and wherein said inhibitor is less
active on at least one other allele of said gene.

73. A method of inhibiting growth of a cell comprising the step of:
administering at least one inhibitor active on an allele of a gene vital for cell
viability or growth,

wherein said gene encodes a product required to maintain cellular nucleotides
at levels compatible with cell growth or survival, and wherein said inhibitor is less
active on at least one other allele of said gene.

74. A method of inhibiting growth of a cell comprising the step of:
administering at least one inhibitor active on an allele of a gene vital for cell
viability or growth,

wherein said gene encodes a product required to maintain the integrity and
function of cellular and subcellular structures, and wherein said inhibitor is less
active on at least one other allele of said gene.

75. A method of inhibiting growth of a cell comprising the step of:
administering at least one inhibitor active on an allele of a gene vital for cell
viability or growth,

wherein said gene is located on a high frequency LOH chromosomal arm
region, and wherein said inhibitor is less active on at least one other allele of said
gene.

76. A method of inhibiting growth of a cell comprising the step of:

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administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, and wherein said inhibitor is less active on at least one other allele of said gene.

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77. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

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identifying a patient heterozygous for a said gene encoding a product required for cell proliferation,

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

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78. The method of claim 77, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

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79. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

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determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required for cell proliferation,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

80. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

5 identifying a patient heterozygous for a said gene encoding a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival,

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

10 81. The method of claim 80, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

15 82. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

20 determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

25 83. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

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identifying a patient heterozygous for a said gene encoding a product required to maintain organic compounds at levels compatible with cell growth or survival;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

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84. The method of claim 83, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

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85. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

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determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain organic compounds at levels compatible with cell growth or survival,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

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86. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

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identifying a patient heterozygous for a said gene encoding a product required to maintain cellular proteins at levels compatible with cell growth or survival ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

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87. The method of claim 86, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

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88. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

10 determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain cellular proteins at levels compatible with cell growth or survival ,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

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89. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

20 identifying a patient heterozygous for a said gene encoding a product required to maintain cellular nucleotides at levels compatible with cell growth or survival ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

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90. The method of claim 89, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

91. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

5 determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain cellular nucleotides at levels compatible with cell growth or survival,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

10 92. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

15 identifying a patient heterozygous for a said gene encoding a product required to maintain the integrity and function of cellular and subcellular structures ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

20 93. The method of claim 91, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

25 94. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

determining whether cancer cells in said patient have undergone LOH of a

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said gene encoding a product required to maintain the integrity and function of cellular and subcellular structures,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

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95. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

10 identifying a patient heterozygous for a said gene located on a high frequency LOH chromosomal arm region ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

15 96. The method of claim 95, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

20 97. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

25 determining whether cancer cells in said patient have undergone LOH of a said gene located on a high frequency LOH chromosomal arm region,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

98. A method of identifying a potential patient for treatment with an inhibitor

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active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

identifying a patient heterozygous for a said gene which has at least two
5 sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

10 99. The method of claim 98, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

15 100. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

20 determining whether cancer cells in said patient have undergone LOH of a said gene which has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

25 101. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required for cell proliferation, wherein said portion comprises a sequence variance site, and wherein said probe

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hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

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102. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

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wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

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103. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

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wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

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104. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required to maintain cellular

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proteins at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

105. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

106. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

107. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or

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viability,

wherein said gene is located on a high frequency LOH chromosomal arm region, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

108. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

109. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 1, 13, 21, 29, 37, 53, 69, 77, and 101, wherein said gene is selected from the group consisting of 14-3-3 Protein TAU, CCNA(G2/Mitotic-Specific Cyclin A), CCNB1(G2/Mitotic-Specific Cyclin B1), CCND1(G1/S-Specific Cyclin D1), CCND2(G1/S-Specific Cyclin D2), CCND3(G1/S-Specific Cyclin D3), Cell division control protein 16, Cell division cycle 2, G1 to S and G2 to M, Cell division cycle 25A, Cell division cycle 25B, Cell division cycle 25C, Cell division cycle 27, Cell division-associated protein BIMB, Cyclin A1(G2/Mitotic-Specific Cyclin A1), Cyclin C(G1/S-Specific Cyclin C), Cyclin G1(G2/Mitotic-Specific Cyclin G), Cyclin G2(G2/Mitotic-Specific Cyclin G), Cyclin H, Cyclin H Assembly, GSPT1(G1 to S phase transition 1), Mitotic MAD2 Protein, MRNP7, RANBP1(RAN binding protein 1), WEE1, Cell Division Protein Kinase 4, CDC28 protein kinase 1, CDC28 protein

kinase 2, M-Phase inducer phosphatase 2, M-phase phosphoprotein, mpp6, PPP1ca(Protein phosphatase 1, catalytic subunit, alpha isoform), STM7-LSB, CENP-F kinetochore protein, Centromere autoantigen C, Centromere protein B (80kD), Centromere protein E (312kD), CHC1(Chromosome condensation 1), Chromatin assembly factor-I p150 subunit, Chromatin assembly factor-I p60 subunit, Chromosome segregation gene homolog CAS, HMG1(High-mobility group (nonhistone chromosomal) protein 1), Minichromosome Maintenance (MCM7), Mitotic centromere-associated kinesin, RMSA1(Regulator of mitotic spindle assembly 1), and SUPT5h(Chromatin structural protein homolog (SUPT5H)).

110. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 2, 14, 22, 30, 39, 55, 70, 80, and 102, wherein said gene is selected from the group consisting of PMCA1 (Calcium Pump), PMCA2 (Calcium Pump), PMCA3 (Calcium Pump), PMCA4 (Calcium Pump), ATP2b1 (Calcium-Transporting ATPase Plasma Membrane), ATP2b2 (Calcium-Transporting ATPase Plasma Membrane), ATP2b4 (Calcium-Transporting ATPase Plasma Membrane), ATP5b (ATP Synthase Beta Chain, Mitochondrial Precursor), Chloride Conductance Regulatory Protein ICLN, H-Erg (Potassium Channel Protein EAG), Nuclear Chloride Ion Channel Protein (NCC27), SCN1b(Sodium Channel, Voltage-Gated, Type I, Beta Polypeptide), Two P-Domain K⁺ Channel TWIK-1, VDAC2 (Voltage-Dependent Anion-Selective Channel Protein 2), ATP1b1 (Sodium/Potassium-Transporting ATPase Beta-1 Chain), ATP1b2 (Sodium/Potassium-Transporting ATPase Beta-2 Chain), ATPase, Ca⁺⁺ transporting, plasma membrane 4, ATPase, Ca⁺⁺ transporting, plasma membrane 2, ATPase, Na⁺/K⁺ transporting, alpha 1 polypeptide, ATPase, Na⁺/K⁺ transporting, alpha 3 polypeptide, ATPase, Na⁺/K⁺ transporting, beta 1 polypeptide, ATPase, Na⁺/K⁺ transporting, beta 2 polypeptide, Na⁺,K⁺ ATPase, 1 Subunit, Na⁺,K⁺ ATPase, 2 alpha, Na⁺,K⁺ ATPase, 3 beta, SLC9a1(Solute carrier family 9 (sodium/hydrogen exchanger)), Solute carrier family 4, anion exchanger, member 1, Solute carrier family 4, anion

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exchanger, member 2, Solute carrier family 9 (sodium/hydrogen exchanger), Passive transporters, MaxiK Potassium Channel Beta Subunit, Chloride Channel 2, Chloride Channel Protein (CLCN7), TRPC1 (Transient Receptor Potential Channel 1), Potassium Channel Kv2.1, ATP5d(ATP synthase, H⁺ transporting, mitochondrial F1 complex, delta subunit), ATP5f1(ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit b), ATP5o(ATP synthase, H⁺ transporting, mitochondrial F1 complex, O subunit), ETFa(Electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)), ETFb(Electron-transfer-flavoprotein, beta polypeptide), Nadh-ubiquinone oxidoreductase 13 kd-B subunit, Nadh-ubiquinone oxidoreductase 39 kD subunit precursor, NADH-Ubiquinone oxidoreductase 75 kD subunit precursor, NADH-Ubiquinone oxidoreductase MFWE subunit, NDUFV2(NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)), Ubiquinol-cytochrome c reductase complex 11 kD, ATP Synthase Alpha Chain, NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit, Ascorbic Acid (transporter), Folate Binding Protein, Folate receptor 1 (adult), Nicotinamide (transporter), Pantothenic Acid transporter, Riboflavin (transporter), SCL19A1 (Solute Carrier Family 19, Member1), Solute carrier family 19 (folate transporter), member 1, Thiamine, B6, B12 (transporter), ATP7b (Copper-Transporting ATPase 2), Ceruloplasmin (ferroxidase), Ceruloplasmin receptor (Copper Transporter), Copper Transport Protein HAH1, Molybdenum, Selenium, Transferrin Receptor (Iron Transporter), Zinc Transporter, and mitochondrial import receptor subunit TOM20.

111. The method ,inhibitor, pharmaceutical composition, or nucleic acid probe of 3, 25, 23, 31, 41, 57, 71, 83, and 103, wherein said gene is selected from the group consisting of GLUT1, GLUT2, GLUT3, GLUT4, GLUT5, GLUT6, Solute carrier family 5 (sodium/glucose cotransporter), Solute carrier family 2 (facilitated glucose transporter), member 2, Solute carrier family 2 (facilitated glucose transporter) member 5, Solute carrier family 3 member 1, System b,(Na⁺ independent), System y,(Na⁺ independent), ATRC1(Catioinc), LEUT(Leucine Transporter),

SLC1A1(Solute Carrier Family 1, Member 1), Solute carrier family 16
 (monocarboxylic acid transporters), ACO1(Aconitase 1), ACO2(Aconitase 2,
 mitochondrial), Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain, Acyl-
 Coenzyme A dehydrogenase, C-4 to C-12 straight chain, Acyl-Coenzyme A
 5 dehydrogenase, long chain, Acyl-Coenzyme A dehydrogenase, very long chain,
 aKGD (alpha ketoglutaratedehydrogenase), ALD-a (Aldolase), ALD-b (Aldolase),
 ALD-c (Aldolase), CS (Citrate Synthetase), Dihydrolipoamide S-succinyltransferase,
 DLAT(Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate
 dehydrogenase complex)), DLD(Dihydrolipoamide dehydrogenase (E3 component
 10 of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto
 acid dehydrogenase complex)), E1k (Oxoglutarate dehydrogenase), E2k
 (Dihydrolipoamide S-succinyltransferase), E3 (Dihydrolipoyl Dehydrogenase),
 ENO1(Enolase 1, alpha), ENO2(Enolase 2), ENO3(Enolase 3), Enolase 2, (gamma,
 neuronal), Enolase 3, (beta, muscle), FH(Fumarate hydratase), G3PDH
 15 (Glyceraldehyde-3-Phosphate Dehydrogenase), G6PD (Glucose-6-Phosphate
 Dehydrogenase), Glucose-6-phosphate dehydrogenase, HK1 (Hexokinase 1), HK2
 (Hexokinase 2), HK3 (Hexokinase 3), IDH1(Isocitrate dehydrogenase 1 (NADP+),
 soluble), IDH2(Isocitrate dehydrogenase 2 (NADP+), mitochondrial),
 MDH1(Malate dehydrogenase 1, NAD (soluble)), MDH2(Malate dehydrogenase 1,
 20 NAD (mitochondrial)), NAD(H)-specific isocitrate dehydrogenase alpha subunit,
 Oxoglutarate dehydrogenase (lipoamide), PDHB (Pyruvate Dehydrogenase),
 PDHB(Pyruvate dehydrogenase (lipoamide) beta), PDK4 (Pyruvate dehydrogenase
 kinase, isoenzyme 4), PFKL(Phosphofructokinase), PGI (Phosphoglucoisomerase),
 PGKa (Phosphoglyceromutase), PGKb (Phosphoglyceromutase), PGM1
 25 (Phosphoglyceromutase), PGM2 (Phosphoglyceromutase), PGM3
 (Phosphoglyceromutase), PGM4 (Phosphoglyceromutase), Phosphofructokinase,
 muscle, Phosphoglucomutase 1, Phosphoglycerate kinase 1, PK1 (Pyruvate Kinase),
 PK2 (Pyruvate Kinase), PK3 (Pyruvate Kinase), Pyruvate dehydrogenase kinase
 isoenzyme 2 (PDK2), Pyruvate kinase, liver, Pyruvate kinase, muscle,

SDH1(Succinate dehydrogenase, iron sulphur (Ip) subunit), SDH2(Succinate dehydrogenase 2, flavoprotein (Fp) subunit), TKT(Transketolase (Wernicke-Korsakoff syndrome)), TPI (Trisephosphate Isomerase), Asparagine Synthetase, Aminoacylase-1, Aminoacylase-2, ACAC (Acetyl CoA Carboxylase Beta), ACAC (Acetyl CoA Carboxylase), ACADSB(Acyl-coA dehydrogenase), Mevalonate kinase, Phosphomevalonate kinase, Aspartoacylase, Ornithine decarboxylase 1, Short-acyl-CoA dehydrogenase, Medium acyl-CoA dehydrogenase, Long acyl-CoA dehydrogenase, Isovaleryl CoA dehydrogenase, 2-methyl branched chain, Adenosine Deaminase, Purine-nucleoside phosphorylase, Guanine Deaminase, Xanthine Oxidase, ITM1 (Integral Transmembrane Protein), GFPT (Glutamine-Fructose-6-Phosphate Transaminase), Heparan, Polypeptide N-Acetyltransferase, ACAA(Acetyl-Coenzyme A acyltransferase), Lysophosphatidic acid acyltransferase-alpha, Lysophosphatidic acid acyltransferase-beta, FNTa (Farnesyltransferase Alpha Subunit), FNTb (Farnesyltransferase Beta Subunit), NMT1 (N-myristoyltransferase), Calcineurin A, Calcineurin B, Calreticulin Precursor, Phosphatase 2b, PPP3ca(Protein phosphatase 3 , catalytic subunit), SNK Interacting 2-28(Calcineurin B Subunit), Protein Kinase C, PRKCA(Protein kinase C, alpha), PRKCB1(Protein kinase C, beta 1), PRKCD(Protein kinase C, delta), PRKCM(Protein kinase C, mu), PRKCQ(Protein kinase C-theta), PRKCSH(Protein kinase C substrate 80K-H), Geranylgeranyl, Geranylgeranyltransferase (Type I Beta), GGTB (Geranylgeranyltransferase), Geranylgeranyltransferase (Type II Beta-Subunit), Gdp Dissociation Inhibitors, GDI Alpha (RAB GDP Dissociation Inhibitor Alpha), and Rab Gdp (RAB GDP Dissociation Inhibitor Alpha).

112. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 4, 16, 24, 32, 43, 59, 72, 86, and 104, wherein said gene is selected from the group consisting of GOT(Glutamic-oxaloacetic transaminase 2), GOT1(Glutamic-oxaloacetic transaminase 1), PYCS(Pyrroline-5-carboxylate synthetase), Tyrosine aminotransferase, AARS, CARS, DARS, EPRS, FARS,

GARS, HARS, IARS, KARS, LARS, MARS, NARS, QARS , RARS, SARS, TARS, VARS, WRS, YARS, Ribosomal Protein L11, Ribosomal Protein L12, Ribosomal Protein L17, Ribosomal Protein L18, Ribosomal Protein L18a, Ribosomal Protein L19, Ribosomal Protein L21, Ribosomal Protein L22, Ribosomal Protein L23, Ribosomal Protein L23a, Ribosomal Protein L25, Ribosomal Protein L26, Ribosomal Protein L27, Ribosomal Protein L27a, Ribosomal Protein L28, Ribosomal Protein L29, Ribosomal Protein L30, Ribosomal Protein L31, Ribosomal Protein L32, Ribosomal Protein L35, Ribosomal Protein L35a, Ribosomal Protein L36a, Ribosomal Protein L39, Ribosomal Protein L4, Ribosomal Protein L41, Ribosomal Protein L44, Ribosomal Protein L6, Ribosomal Protein L7, Ribosomal Protein L7a, Ribosomal Protein L8, Ribosomal Protein L9, Ribosomal Protein P1, Ribosomal Protein S10, Ribosomal Protein S11, Ribosomal Protein S13, Ribosomal Protein S14, Ribosomal Protein S15, Ribosomal Protein S15A, Ribosomal Protein S16, Ribosomal Protein S17, Ribosomal Protein S17A, Ribosomal Protein S17B, Ribosomal Protein S18, Ribosomal Protein S20, Ribosomal Protein S20A, Ribosomal Protein S20B, Ribosomal Protein S21, Ribosomal Protein S23, Ribosomal Protein S25, Ribosomal Protein S26, Ribosomal Protein S28, Ribosomal Protein S29, Ribosomal Protein S3, Ribosomal Protein S3A, Ribosomal Protein S4, Ribosomal Protein S4X, Ribosomal Protein S4Y, Ribosomal Protein S5, Ribosomal Protein S6, Ribosomal Protein S7, Ribosomal Protein S8, Ribosomal Protein S9, Initiation of polypeptide polymerization, eIF-2 (Eukaryotic initiation factor), eIF-2-associated p67(Eukaryotic initiation factor), eIF-2A(Eukaryotic initiation factor), eIF-2Alpha(Eukaryotic initiation factor), eIF-2B(Eukaryotic initiation factor), eIF-2B-Gamma(Eukaryotic initiation factor), eIF-2Beta(Eukaryotic initiation factor), eIF-3 p110(Eukaryotic initiation factor), eIF-3 p36(Eukaryotic initiation factor), eIF-4A(Eukaryotic initiation factor), eIF-4C(Eukaryotic initiation factor), eIF-4E(Eukaryotic initiation factor), eIF-4Gamma(Eukaryotic initiation factor), eIF-5(Eukaryotic initiation factor), eIF-5A, Eukaryotic peptide chain release factor subunit 1, P97(Eukaryotic initiation factor), eEF1A2(Eukaryotic elongation factor),

eEF1D(Eukaryotic elongation factor), eEF2(Eukaryotic elongation factor), eIF4A2 (Eukaryotic initiation factor), KIAA0031(Elongation factor 2), KIAA0219(Putative translational activator C18G6.05C), Factor 1-Alpha 2(Eukaryotic translation elongation factor 1 alpha 2), Cis-Trans Isomerase, DNAJ Protein Homolog 1, DNAJ Protein Homolog 2, DNAJ Protein homolog HSJ1, T-Complex, Aspartylglucosaminidase, T-Complex 1, Alpha, T-Complex 1, Epsilon, T-Complex 1, Gamma, T-Complex 1, Theta, T-Complex 1, Zeta, 26S Protease regulatory subunit 4, Alpha-2-Macroglobulin, Calpain 1, Large, CLPP(ATP-Dependent CLP protease proteolytic subunit), KIAA0123 (Mitochondrial processing peptidase alpha subunit), MMP7, Proteasome Beta 6, Proteasome Beta 7, Proteasome C13, Proteasome C2, Proteasome C7-1, Proteasome inhibitor hPI31 subunit, Proteasome P112, Proteasome P27, Proteasome P55, Enzyme E2-17 Kd(Cyclin-selective ubiquitin carrier protein), ISOT-3(Ubiquitin carboxyl-terminal hydrolase T), ORF (Ubiquitin carboxyl-terminal hydrolase 14), PGP(Ubiquitin carboxyl-terminal hydrolase isozyme L1), UBA52(Ubiquitin A-52 residue ribosomal protein fusion product 1), Ubiquitin carboxyl-terminal hydrolase 3, Ubiquitin carboxyl-terminal hydrolase isozyme L3, Ubiquitin carboxyl-terminal hydrolase T, Ubiquitin carrier protein (E2-EPF), Ubiquitin fusion-degradation protein (UFD1L), Ubiquitin Hydrolase, Ubiquitin-conjugating enzyme E2I, SEC23(Protein transport protein SEC23), SEC23A(Protein transport protein SEC23), SEC7(Protein transport protein SEC7), SEC61 (Beta Subunit), and LDLR (LDL receptor).

113. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 5, 17, 25, 33, 45, 73, 89, and 105, wherein said gene is selected from the group consisting of Adenylate Kinase-2, Adenylosuccinate synthetase, Adenylosuccinate Lyase, DPRT (ADP-Ribosyltransferase), ADSL (Adenylosuccinate lyase/AMP synthetase), ADSS (Adenylosuccinate Synthetase), CAD PROTEIN, CTP Synthetase, CTPS(CTP synthetase), Cytidine Triphosphate Synthetase, GARS (Phosphoribosylglycinamide synthetase), GART (Phosphoribosylglycinamide

formyltransferase), GART(Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase), GMP Synthetase, IMP Cyclohydrolase, IMP dehydrogenase, IMPDH1(IMP (inosine monophosphate) dehydrogenase 1), IMPDH2(IMP (inosine monophosphate) dehydrogenase 2), Phosphoribosyl diphosphotransferase, Phosphoribosylaminoimidazolecarboxamide formyltransferase, Phosphoribosylformylglycinamide synthetase, Phosphoribosylglycinamide carboxylase, Phosphoribosylglycinamide-succinocarboxamide synthetase, PPAT (Amidophosphoribosyltransferase), PPAT(Phosphoribosyl pyrophosphate amidotransferase), Ribonucleoside-diphosphate reductase M1 chain, Ribonucleoside-diphosphate reductase M2 chain, Thymidine Kinase, Thymidylate Synthase, UMK(Uridine kinase), UMPK (Uridine monophosphate kinase), UMPS(Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)), Uridine Phosphorylase, DNA Origin Recognition Complex, ORC1, ORC2, ORC3, ORC4, ORC5, ORC6, ORC Regulators, CDC6, CDC7, CDC1, DNA Polymerization, DNA Polymerases, Adprt (NAD(+) ADP-Ribosyltransferase), DNA Polymerase Alpha-Subunit, DNA Polymerase Delta, POLa(DNA Polymerase Alpha/Primase Associated Subunit), POLb(DNA Polymerase Beta Subunit), POLd1(Polymerase (DNA directed), Delta 1, Catalytic Subunit), POLd2(Polymerase (DNA directed), Delta 2), POLE(Polymerase (DNA directed)), POLg (DNA Polymerase Gamma Subunit), Terminal Transferase (DNA Nucleotidylexotransferase), Activator 1 36 Kd, CDC46 (DNA Replication Licensing Factor), CDC47 (DNA Replication Licensing Factor CDC47), DNA Topoisomerase III, DRAP1 (DNA Replication Licensing Factor MCM3), KIAA0030 Gene (Cell Division Control Protein 19), KIAA0083 Gene (DNA Replication Helicase DNA2), MCM3 (DNA Replication Licensing Factor MCM3), PCNA (Proliferating Cell Nuclear Antigen), PRIM1 (DNA Primase 49 kD Subunit), PRIM2 (DNA Primase), PRIM2a (DNA Primase 58 kD Subunit), PRIM2b (DNA Primase), RECa (Replication Protein A 14 kD Subunit), RFC1 (Replication Factor C (activator 1) 1),

RFC2 (Replication Factor C 2), RFC3 (Replication Factor C (activator 1) 3), RFC4
 (Replication Factor C, 37-kD subunit), RFC5 (Replication Factor C), RPA1
 (Replication protein A1 (70kD)), RPA2 (Replication protein A2 (32kD)), RPA3
 (Replication protein A3 (14kD)), TOP1 (DNA Topoisomerase I), TOP2a
 5 (Topoisomerase (DNA) II Alpha (170kD)), TOP2b (Topoisomerase (DNA) II Beta
 (180kD)), CHL1(CHL1-Related Helicase), DNA Helicase II, Mi-2(Chromodomain-
 Helicase- DNA-Binding Protein CHD-1), RECQL (ATP-Dependent DNA Helicase
 Q1), Smbp2 (DNA-Binding Protein SMUBP-2), H1(0) (Histone H5A), Histone H1d,
 Histone H1x, Histone H2a.1, Histone H2a.2, Histone H2b.1, Histone H4, SLBP
 10 (Histone Hairpin-Binding Protein), TATA-binding Complex, Small Nuclear RNA-
 Activating Complex, Polypeptide 1, 43KD (SNAPC1), Small Nuclear RNA-
 Activating Complex, Polypeptide 2, (SNAPC2), Small Nuclear RNA_Activating
 Complex, Polypeptide 3, 50KD (SNAPC3), TAF2D(TBP-associated factor),
 TAFII100(TBP-associated factor), TAFII130(TBP-associated factor), TAFII20(TBP-
 15 associated factor), TAFII250(TBP-associated factor), TAFII28(TBP-associated
 factor), TAFII30(TBP-associated factor), TAFII32(TBP-associated factor),
 TAFII40(TBP-associated factor), TAFII55(TBP-associated factor), TAFII80(TBP-
 associated factor), TBP(TATA Binding Protein), TMF1 (TATA Element Modulatory
 Factor 1), RPB 7.0, RPB 7.6, RPB 17, RPB 14.4, RNA polymerase I subunit
 20 hRPA39, 13.6 Kd Polypeptide (DNA-Directed RNA Polymerase II 13.6 kD
 Polypeptide), POLR2C(RNA polymerase II, polypeptide C (33kD)), Polypeptide A
 (220kd), RNA Polymerase II 23k, RNA polymerase II holoenzyme component
 (SRB7), RNA polymerase II subunit (hsRPB10), RNA polymerase II subunit
 (hsRPB8), RNA polymerase II subunit hsRPB4, RNA polymerase II subunit
 25 hsRPB7, RNA Polymerase II Subunit(DNA- Directed RNA Polymerases I, II, and
 III 7.3 kD polypeptide), TCEB1L(Transcription elongation factor B (SIII),
 polypeptide 1-like), RNA polymerase III subunit (RPC39), RNA polymerase III
 subunit (RPC62), Elongation Factor 1-Beta, Elongation Factor S-II, TCEA (110kD),
 TCEB1, TCEB (18kD), TCEB1L, TCEB3, TCEC (15kDa), TFIIS (Transcription

Elongation Factor IIS), E2F1 (E2F Transcription Factor), TFAP2A (Transcription
 Factor A2 Alpha), TFCEP2 (Transcription Factor CP2), TFC12 (Transcription Factor
 12), PRKDC (Protein Kinase, DNA activated catalytic subunit), SUPT6H, TFIIA
 gamma subunit, TFIIA delta, TFIIB related factor hBRF (HBRF), TFIIE Alpha
 5 Subunit, TFIIE Beta Subunit, TFIIF, Beta Subunit, GTF2F1 (TFIIF), GTF2F2
 (TFIIF), General Transcription Factor IIIA, TFIIH(52 kD subunit of transcription
 factor), TFIIH(p89), TFIIH(p80), TFIIH(p62), TFIIH(p44), TFIIH(p34),
 Transcription Factor IIf(General transcription factor IIF, polypeptide 1 (74kD
 subunit))Transcription Factor IIf(General transcription factor IIF, polypeptide 1
 10 (74kD subunit)), BTf 62 kDSubunit (Basic transcription factor 62 kD subunit),
 CAMP-dependent transcription factor ATF-4, CCAAT box-binding transcription
 factor 1, CRM1(Negative regulator CRM1), Cyclic-AMP-dependent transcription
 factor ATF-1, GABPA(GA-binding protein transcription factor, alpha subunit
 (60kD)), ISGF-3(Signal transducer and activator of transcription 1-alpha/beta),
 15 NFIX(Nuclear factor I/X (CCAAT-binding transcription factor)), NFYA(Nuclear
 transcription factor Y, alpha), NTF97(Nuclear factor p97), Nuclear factor I-B2
 (NFIB2), Nuclear factor NF45, Nuclear factor NF90, POU2F1(POU domain, class
 2, transcription factor 1), Sp2 transcription factor, TCF12(Transcription factor 12
 (HTF4, helix-loop-helix transcription factors 4)), TCF3(Transcription factor 3 (E2A
 20 immunoglobulin enhancer binding factors E12/E47)), TCF6L1(Transcription factor
 6-like 1), TF P65(Transcription factor p65), TFCOUP2(Transcription factor COUP
 2 (a.k.a. ARP1)), Transcription factor IL-4 Stat, Transcription Factor S-II
 (Transcription factor S-II-related protein), Transcription factor Stat5b, Transcription
 Factor, Transcription factor (CBFB), 9G8 Splicing Factor (Pre-mRNA Splicing
 25 factor SRP20), CC1.3(Splicing factor (CC1.3)), HnRNP F protein,
 HNRPA2B1(Heterogeneous nuclear ribonucleoproteins A2/B1),
 HNRPG(Heterogeneous nuclear ribonucleoprotein G), HNRPK(Heterogeneous
 nuclear ribonucleoprotein K), Pre-mRNA splicing factor helicase, Pre-mRNA
 splicing factor SF2, P33 subunit, Pre-mRNA splicing factor SRP20, Pre-mRNA

splicing factor SRP75, PRP4(Serine/threonine-protein kinase PRP4), PTB-Associated
 Splicing Factor, Ribonucleoprotein A', Ribonucleoprotein A1, Ribonucleoprotein
 C1/C2, RNP Protein, L (Heterogeneous nuclear ribonucleoprotein L), RNP-Specific
 C(U1 small nuclear ribonucleoprotein C), SAP 145(Spliceosome associated protein
 5), SAP 61(Splicesomal protein), SC35(Splicing factor), SF3a120, SFRS2(Splicing
 factor, arginine/serine-rich 2), SFRS5(Splicing factor, arginine/serine-rich 5),
 SFRS7(Splicing factor, arginine/serine-rich 7), Small nuclear ribonucleoprotein SM
 D1, SnRNP core protein Sm D2, SnRNP core protein Sm D3, SNRP70(U1 snRNP
 70K protein), SNRPB(Small nuclear ribonucleoprotein polypeptides B and B1),
 10 SNRPE(Small nuclear ribonucleoprotein polypeptide E), SNRPN(Small nuclear
 ribonucleoprotein polypeptide N), Splicing factor SF3a120, Splicing factor U2AF
 35 kD subunit, Splicing factor U2AF 65 kD subunit, SRP30C(Pre-mRNA splicing
 factor SF2, p33 subunit), SRP55-2(Pre-mRNA splicing factor SRP75), Transcription
 factor BTEB, Transcription initiation factor TFIID 250 kD subunit, Cleavage and
 15 polyadenylation specificity factor, Cleavage stimulation factor, 3' pre-RNA, subunit
 1, 50kD, Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD, HNRNP
 Methyltransferase, PABPL1(Poly(A)-binding protein-like 1), Pap mRNA(Poly(A)
 Polymerase), RNA unwinding, RNA Helicase, GU Protein (ATP-Dependent RNA
 helicase dead), KIAA0224 Gene(Putative ATP-dependent RNA helicase), RNA
 20 Helicase A, RNA Helicase P110, and Ste13(Nuclear RNA Helicase).

114. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of
 any of claims 6, 18, 26, 34, 47, 63, 92, and 106, wherein said gene is selected from
 the group consisting of AP47(Clathrin Coat Assembly AP47), AP50(Clathrin Coat
 25 Assembly Protein AP50), Cell Surface Protein (Clathrin Heavy Polypeptide-Like
 Protein), Cltb(Clathrin Light Chain B), Cltc (Clathrin Heavy Chain), Adenylate
 Cyclase, Adenylate Cyclase, Adenylate Cyclase, II, Adenylate Cyclase,IV, Complex
 I, MTND1 (Subunit ND1), MTND2 (Subunit ND2), MTND3 (Subunit ND3),
 MTND4 (Subunit ND4), MTND4L (Subunit ND4L), MTND5 (Subunit ND5),

MTND6 (Subunit ND6), Complex II, Complex III, Cytochrome b subunit, Complex
 IV, CO1 (Cytochrome c Oxidase Subunit I), CO2 (Cytochrome c Oxidase Subunit
 2), CO3 (Cytochrome c Oxidase Subunit 3), Complex V, ATP Synthase Subunit
 ATPase 6, Kinesin Heavy Chain, Kinesin Light Chain, Syntaxin 1a, Syntaxin 1b,
 5 Syntaxin 3, Syntaxin 5a, Syntaxin 7, CANX (Calnexin), ER Lumen Protein 1, ER
 Lumen Protein 2, Ribophorin I, Ribophorin II, Signal recognition particle receptor,
 SRP Protein, TIM17 preprotein translocase, Golgin-245, TGN46 (Trans-Golgi
 Network Integral Membrane Protein TGN38 Precursor), Beta-Cop, Coatomer Beta'
 Subunit, Coatomer Delta Subunit, Gp36b Glycoprotein (Vesicular integral-membrane
 10 protein VIP36 precursor), Homologue of yeast sec7, Protein transport protein SEC13
 (Chromosome 3p25), SEC14 (*S. Cerevisiae*), Synaptic vesicle membrane protein
 VAT-1, Synaptobrevin-3, Synaptotagmin I, Transmembrane(COP-coated vesicle
 membrane protein p24 precursor), Vacuolar-Type (Clathrin-coated vesicle/synaptic
 vesicle proton pump 116 kd subunit), 140 kD Nucleolar phosphoprotein,
 15 Autoantigen p542, Export protein Rae1 (RAE1), Heterogeneous nuclear
 ribonucleoprotein A1, Nuclear pore complex protein hnup153, Nuclear pore complex
 protein NUP214, Nuclear pore glycoprotein p62, Nuclear Transport Factor 2,
 Nucleoporin 98 (NUP98), NUP88, Ribonucleoprotein A, Ribonucleoprotein B",
 Karyopherin, Importin Alpha Subunit, TRN (Transportin), Actin, Beta-Contractin,
 20 Capping Protein Alpha, CFL1 (Cofilin, Non-Muscle Isoform), Desmin, Dystrophin,
 Gelsolin, hOGG1(Myosin Light Chain Kinase), IC Heavy Chain, Itga2 (Integrin,
 Alpha 2 (CD49B, alpha 2 Subunit of VLA-2 receptor)), Itga3 (Integrin Alpha-3
 Precursor), Keratin 19, Keratin, Type II, Lamin A, LBR(Lamin B Receptor), Light
 Chain Alkali, MacMarcks mRNA, MAP1a (Microtubule-Associated Protein 1A),
 25 MAP2(Microtubule-Associated Protein 2), MEG1(Protein-Tyrosine Phosphatase
 MEG1), Microtubule-Associated Protein TAU, Suppressor Of Tubulin STU2, TUBg
 (Tubulin Gamma Chain), Tubulin Alpha-4 Chain, USH1b (Myosin II Heavy Chain),
 Villin, Villin 2 (Ezrin), Actin Depolymerizing, Capping (Actin Filament),
 MYH9(Myosin, Heavy Polypeptide 9, Non-Muscle), MYL5(Myosin Regulatory

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Light Chain 2), Myosin Heavy Chain 95F, Myosin Heavy Chain IB, Myosin IB, Sh3p17(Myosin IC Heavy Chain), Sh3p18(Myosin IC Heavy Chain), KIAA0059(Dematin:Actin-Bundling Protein), TTN (Titin:Myosin Light Chain Kinase), ATP6c(Vacuolar H⁺ ATPase proton channel subunit), ATP6a1 (ATPase, H⁺ Transporting, Lysosomal (Vacuolar Proton Pump), Alpha Polypeptide, 70kD), ATP6b1(ATPase, H⁺ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD), ATP6d(ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 42kD), ATP6e(ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 31kD), ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 31kD, and Superoxide Dismutase.

115. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a conditionally essential gene, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

(a) determining at least two alleles of a said gene;

(b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles; wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

116. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a conditionally essential gene, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

117. A pharmaceutical composition, comprising

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at least one allele specific inhibitor targeting at least one but less than all allelic forms of a conditionally essential gene in a population; and
a pharmaceutically acceptable carrier or excipient.

5 118. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a conditionally essential gene having at least two alternative alleles, comprising the steps of:

10 (a) identifying a conditionally essential gene that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

15 (c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in whom cancerous cells have only an allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene and contain an allelic form not inhibited by said inhibitor.

20 119. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. subjecting cells of said precancerous condition to an altered condition such that a first conditionally essential becomes essential;

25 b. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of said first conditionally essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells; and

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wherein cells of said precancerous condition have undergone LOH of said first gene.

120. The method of claim 119, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

c. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of a conditionally essential gene or an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different gene, and wherein said patient is heterozygous for each targeted gene and each targeted gene has undergone LOH in cells of said precancerous condition.

121. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a conditionally essential gene, comprising the steps of:

a) subjecting cells of said cancer to altered conditions such that said gene is essential; and

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

122. The method of claim 121, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular conditionally essential gene; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

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123. A method of inhibiting growth of a cell comprising the steps of:

- a) subjecting said cell to conditions such that said gene is essential; and
- b) administering at least one inhibitor active on an allele of said

conditionally essential gene,

5 wherein said inhibitor is less active on at least one other allele of said gene.

124. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a conditionally essential gene, wherein said patient is suffering from a cancer, said method comprising the step of:

10 identifying a patient heterozygous for a said gene,

 wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

125. The method of claim 124, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

15 wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

126. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a conditionally essential gene, wherein said patient is suffering from a cancer, said method comprising the step of:

20 determining whether cancer cells in said patient have undergone LOH of a said gene,

 wherein if said cells have undergone LOH of said gene, then said patient is
25 a potential patient for said treatment.

126. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a conditionally essential gene, wherein said portion comprises a sequence variance site, and wherein

said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

5 127. A method for selecting a patient for treatment with an antiproliferative treatment, comprising the steps of:

a) determining whether normal somatic cells in a potential patient are heterozygous for an essential or conditionally essential gene, wherein a first allelic form of said gene is more active than a second allelic form, and wherein a reduction
10 in the activity of said gene in a cell increases the sensitivity of said cell to a said antiproliferative treatment; and

b) determining whether cancer cells of said patient have only said second allelic form of said gene,

wherein if said somatic cells are heterozygous and said cancer cells have only
15 said second allelic form, it is indicative that said patient is suitable for treatment with said antiproliferative treatment.

128. A method for selecting an antiproliferative treatment for a patient suffering from a cancer, comprising the steps of:

20 a) determining whether normal somatic cells in a potential patient are heterozygous for an essential or conditionally essential gene which reduces the sensitivity of cells to an antiproliferative treatment, wherein a first allelic form of said gene is more active than a second allelic form, and wherein a reduction in the activity of said gene in a cell increases the sensitivity of said cell to a said antiproliferative
25 treatment; and

b) determining whether cancer cells of said patient have only said second allelic form of said gene,

wherein if said somatic cells are heterozygous for said gene and said cancer cells have only said second allelic form, it is indicative that said antiproliferative

treatment is suitable for said patient.

129. The method of any of claims 115-129, wherein said gene is selected from the group consisting of:

5 galactose-1-phosphate uridylyltransferase, galactose kinase, UDP galactose-4-epimerase, methionine synthase, asparagine synthase, glutamine synthetase, multidrug resistance gene/Pglycoprotein, multidrug resistance associated proteins 1-5, bleomycin hydrolase, dihydropyrimidine dehydrogenase, β -ureidopropionase, β -alanine synthetase, cytidine deaminase, thiopurine methyltransferase, CYP1A1, CYP1A2, 10 CYP2A6, CYP2A7, CYP2B6, CYP2B7, CYP2C8, CYP2C9, CYP2C17, CYP2C18, CYP2C19, CYP2D6, CYP2E1, CYP2F1, CYP3A3, CYP3A4, CYP3A5, CYP3A7, CYP4B1, CYP7, CYP11, CYP17, CYP19, CYP21, CYP27, glutathione transferase alpha, glutathione transferase theta, glutathione transferase mu, glutathione transferase pi, methylguanine methyltransferase, 3-alkylguanine alkyltransferase, 3-methyladenine 15 DNA glucosylase, DNA dependent protein kinase, catalytic subunit of DNA-PK, DNA binding subunit of DNA-PK Ku-70 or Ku-80 subunit, KARP-1, Poly(ADP-ribose) polymerase, Fanconi Anemia genes A, B, C, D, E, F, G, and H, ERCC-1, ERCC2/XPD, ERCC3/XPB, ERCC4, ERCC5, ERCC6, XPA, XPC, XPE, HHR23A, HHR23B, uracil glycosylase, 3-methyl adenine DNA glycosylase, NF-kappa B, 20 XRCC4, XRCC5/Ku80, XRCC6, XRCC7, glutathione-S-transferase, I-kappa B alpha, HSP70, HSP27, and 9-oxoguanine DNA glycosylase.

131. A method for identifying a potential patient undergoing transplantation for treatment with an inhibitor active on at least one but less than all alleles of an 25 essential gene, comprising the step of:

identifying a patient undergoing an allogenic bone marrow transplantation in which the donor tissue contains at least one alternative allele of an essential gene different from the alleles in somatic cells of said patient.

132. The method of claim 131, wherein said donor or said recipient is homozygous for an alternative allelic form of an essential gene that is not present in the other of said donor or said recipient.

5 133. A method for treating graft versus host disease in a patient receiving allogenic bone marrow transplantation, said method comprising the step of

administering to said patient at least one allele specific inhibitor specific for at least one but less than all of the allelic forms of an essential gene in a population, wherein said inhibitor inhibits stimulation of the donor immune system, and cells of
10 the said patient comprise an allelic form of said gene not present in the donor bone marrow.

134. The method of claim 133, wherein said allele specific inhibitor is selected by identifying at least one alternative alleles of an essential gene present in the donor
15 tissues but absent in the normal somatic cells of said patient; and

selecting a said inhibitor active on a said alternative allele of an essential gene present in said donor tissues but absent in the normal somatic cells of said patient.

20 135. The method of claim 134, wherein said at least one inhibitor recognizes both alleles of said essential gene that are present in said donor, but not both alleles of said gene that are present in said patient.

25 136. A method for enhancing engraftment of an allogenic bone marrow transplant, comprising the step of administering to a patient receiving said transplant an allele specific inhibitor which kills or suppresses the patient's bone marrow but not the donor bone marrow, thereby providing space for engraftment of the donor cells within the marrow cavity.

137. The method of claim 136, wherein the allele specific inhibitor is selected by

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identifying alternative alleles of an essential gene that are present in the recipient but not the donor marrow.

5 138. The method of claim 137, wherein said allele specific inhibitor recognizes both allelic forms of the essential gene that are present in the recipient, but not both allelic forms of the same gene that are present in the recipient.

139. A method for treating or preventing chimerism in allogenic bone marrow transplantation, comprising
10 selectively killing or suppressing proliferation of the patient's own cells without toxicity to the donor cells by
administering to a patient receiving said transplantation at least one allele specific inhibitor active on at least one but less than all alternative alleles of a gene vital for cell growth or viability, wherein said inhibitor targets the allelic form or
15 forms of a gene in bone marrow of said patient but does not target at least one allelic form of said gene in the donor bone marrow.

140. A method for treating cancer in a patient receiving allogenic or autologous transplantation, comprising the step of
20 administering to said patient at least one allele specific inhibitor which kills or inhibits the growth of cancer cells without toxicity to the transplanted marrow.

141. The method of claim 141, wherein said transplantation is autologous transplantation and said at least one allele specific inhibitor is selected to be active
25 on the allele of an essential gene remaining in the cancer cells due to LOH in patients whose normal somatic cells are heterozygous for said essential gene, but not on the alternative allele of said gene present in said normal somatic cells,
whereby said administration enables continuing therapy of cancer without suppression of the transplanted marrow.

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142. The method of claim 140, wherein said transplantation is allogenic transplantation and said allele specific inhibitor recognizes both alleles of said essential gene that are present in the recipient, but not both forms of the said gene that are present in said patient.

5

143. A method for eliminating malignant cells from transplanted marrow during autologous transplantation of a patient heterozygous for an essential gene, comprising

10 contacting cells from harvested autologous bone marrow *ex vivo* with at least one allele specific inhibitor active on at least one but less than all alternative alleles of said essential gene, wherein said inhibitor targets an allelic form of said gene present in cancer cells of said patient but does not target an alternative allele of said gene present in normal cells from said autologous bone marrow,

 wherein said gene has undergone LOH in cancer cells of said patient.

15

144. The method of claim 143, wherein said autologous bone marrow is harvested from said patient prior to high dose radiation or chemotherapy.

145. The method of claim 143, further comprising the steps of:

20

a. identifying one alternative allele of an essential gene remaining in the cancer cell due to LOH in patients who are heterologous with two different alternative forms of the essential gene in normal cells of the autologous bone marrow;

25

b. cultivating said autologous bone marrow *ex vivo* in the presence of an allele specific inhibitor that inhibits the allele that is present in the cancer cells, but not the heterologous allele that is present in the normal bone marrow. .

146. The method of claim 143, wherein said autologous bone marrow is contacted with a plurality of said allele specific inhibitors.

147. A method for separating a first cell from a mixture of cells, comprising the steps of:

a) providing an allele specific binding compound which binds to at least one but less than all alleles of a gene, wherein a said allele of said gene expressed in said first cell is not expressed in other cells of said mixture of cells or is expressed in other cells in said mixture of cells and not in said first cell;

b) contacting said mixture of cells with said binding compound under conditions such that said binding compound binds to said allele and not to non-target alleles; and

c) separating bound cells from unbound cells.

148. The method of claim 147, wherein said mixture of cells comprises normal somatic cells and cancer cells from a patient, said first cells are said normal somatic cells, and said first cells express a said allele deleted in said cancer cells due to LOH of said gene, comprising

separating said normal somatic cells from said cancer cells.

149. The method of claim 147, wherein said allele specific binding compound is an antibody or antibody fragment.

150. The method of claim 147, wherein said binding compound is attached to a solid support.

Fig. 1

bold nucleotide is the polymorphic base

314198

[illegible]

Target Gene Summary Table
Alanyl-tRNA Synthetase
Chromosome 16q22
VARIA304

[illegible]

Fig. 2

SSCP Overview

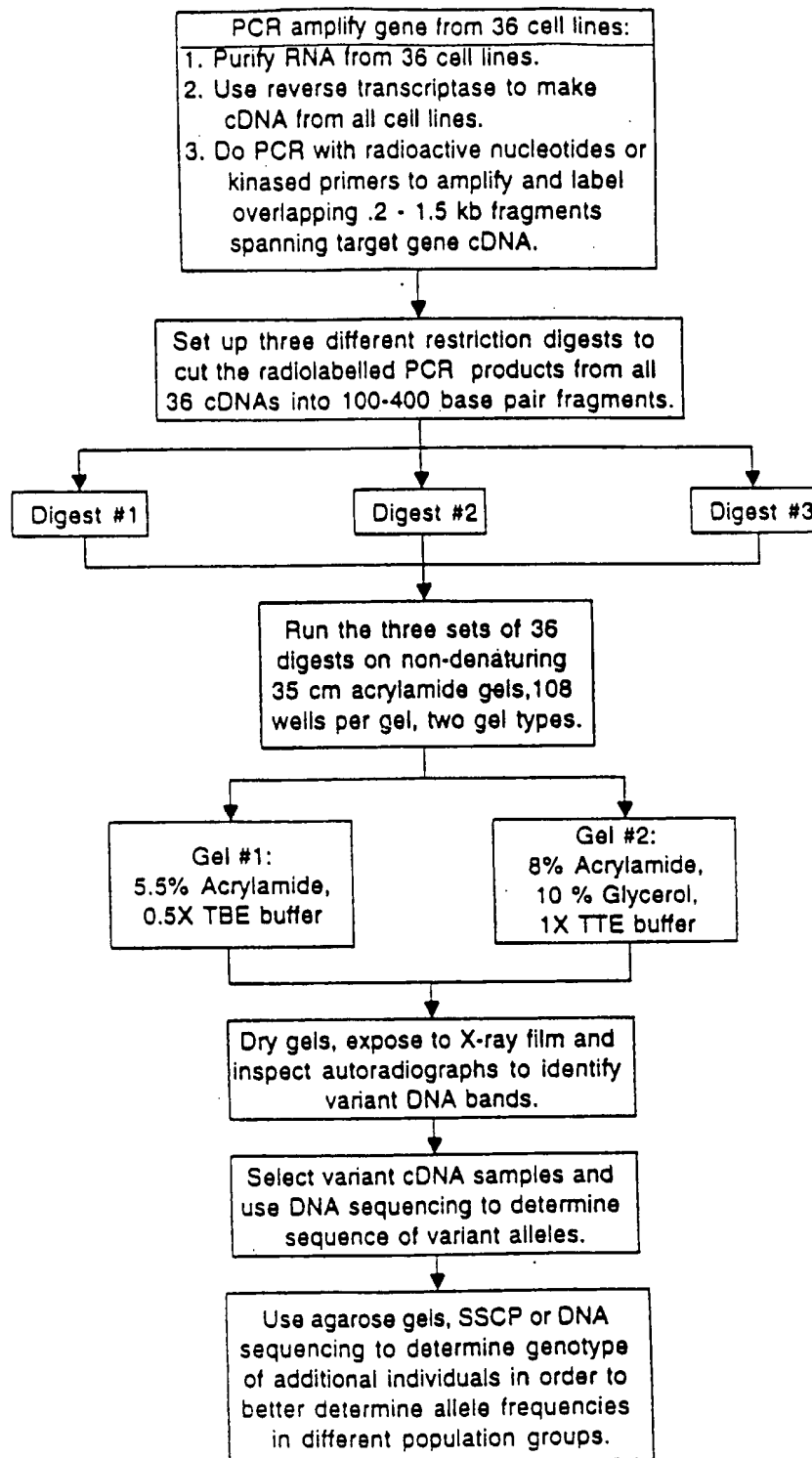


Fig. 3

Chromosome 1 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
36	D1Z2	110	24	0.22	Breast	GCC 5:310
36	D1Z2	37	15	0.41	Breast	AJHG 45:73
36	D1Z2	18	9	0.5	Endocrine	CR 52:770
36	D1Z2	20	1	0.05	Endocrine	CR 52:770
36	D1Z2	7	7	1	Neuroblastom	CR 55:5366
36	D1S243	43	10	0.23	Breast	CR 55:1752
36	D1S243	20	6	0.3	Endocrine	Unknown
36	D1S243	14	14	1	Neuroblastom	CR 55:5366
36	D1S243	36	9	0.25	Neuroblastom	CR 55:5366
36	D1S243	8	7	0.88	Neuroblastom	GCC 10:275
36-35	D1S80	9	0	0	Brain	CR 54:1397
36-35	D1S80	14	1	0.07	Brain	CR 54:1397
36-35	D1S80	34	16	0.47	Brain	AJP 145:1175
36-35	D1S80	17	4	0.24	Breast	GCC 12:16
Unknown	D1S80	74	22	0.3	Breast	CR 53:1990
36-35	D1S80	63	20	0.32	Breast	CR 54:4274
36-35	D1S80	40	8	0.2	Endocrine	GCC 13:9
36-35	D1S80	13	10	0.77	Neuroblastom	GCC 10:275
36-35	D1S80	38	9	0.24	Neuroblastom	CR 55:5681
Unknown	D1S80	19	2	0.11	Testis	CR 54:6265
Unknown	D1S80	17	2	0.12	Testis	CR 9:2245
36.3-35	D1S76	34	16	0.47	Brain	AJP 145:1175
36.3-35	D1S76	41	4	0.1	Breast	CR 53:4356
36.3-35	D1S76	19	3	0.16	Breast	GCC 12:16
36.3-35	D1S76	38	13	0.34	Breast	CR 54:4274
36.3-35	D1S76	17	15	0.88	Neuroblastom	GCC 10:275
Unknown	D1S77	21	10	0.48	Brain	AJP 145:1175
Unknown	D1S77	19	3	0.16	Breast	GCC 12:16
Unknown	D1S77	18	4	0.22	Esophageal	GCC 10:177
Unknown	D1S77	6	2	0.33	Stomach	BJC 73:424
Unknown	D1S253	17	3	0.18	Leukemia	CR 55:5377
36	D1S47	32	3	0.09	Breast	CR 51:1020
36	D1S47	15	1	0.07	Colon	CR 52:285
36	D1S47	17	12	0.71	Colon	CR 50:7232
36	D1S47	24	7	0.29	Melanoma	PNAS 86:1614
36	D1S47	31	7	0.23	Neuroblastom	GCC 10:30
36	D1S214	43	6	0.14	Breast	CR 55:1752
36	D1S214	11	10	0.91	Neuroblastom	GCC 10:275

Chromosome 1 - p Arm

36	D1S214	13	0	0	Stomach	BJC 73:424
Unknown	D1S160	17	9	0.53	Brain	AJP 11145:11
Unknown	D1S160	21	5	0.24	Liver	CR 54:4188
Unknown	D1S160	34	8	0.24	Neuroblastom a	CR 55:5681
Unknown	D1S160	41	22	0.54	Ovary	BJC 75:1105
Unknown	D1S244	36	9	0.25	Neuroblastom a	CR 55:5681
36	D1S450	37	8	0.22	Breast	CR 55:1752
Unknown	NPPA	1	0	0	Testis	GCC 13:249
Unknown	EGD	10	1	0.1	Testis	GCC 13:249
36	D1S228	40	5	0.12	Breast	CR 55:1752
36	D1S228	7	5	0.71	Neuroblastom a	GCC 10:275
36	D1S228	31	7	0.23	Neuroblastom a	CR 55:5681
36	D1S228	8	1	0.12	Stomach	BJC 73:424
Unknown	D1S170	19	5	0.26	Liver	CR 54:4188
Unknown	D1S170	36	7	0.19	Neuroblastom a	CR 55:5681
Unknown	D1S170	33	16	0.48	Ovary	BJC 75:1105
Unknown	D1S94	19	12	0.63	Colon	CR 50:7232
Unknown	D1S94	8	4	0.5	Neuroblastom a	0 7:1185
Unknown	D1S94	36	9	0.25	Neuroblastom a	GCC 10:30
35	D1S199	50	9	0.18	Breast	CR 55:1752
35	D1S199	30	4	0.13	Cervix	CR 56:197
35	D1S199	14	13	0.93	Neuroblastom a	CR 55:5366
35	D1S199	4	2	0.5	Neuroblastom a	GCC 10:275
35	D1S199	9	0	0	Stomach	BJC 73:424
36.1-p34	ALPL	17	2	0.12	Colon	CR 52:285
36.1-p34	ALPL	2	1	0.5	Endocrine	CR 52:770
36.1-p34	ALPL	17	4	0.24	Melanoma	PNAS 86:4614
36.11	D1S112	1	1	1	Neuroblastom a	CR 55:5366
Unknown	D1S112	20	1	0.05	Neuroblastom a	GCC 10:275
Unknown	FUCA1	15	5	0.33	Brain	AJP 1145:117
Unknown	FUCA1	13	6	0.46	Melanoma	PNAS 86:4614
Unknown	FUCA1	14	0	0	Testis	GCC 13:249
Unknown	D1S234	10	8	0.8	Neuroblastom a	GCC 10:275
36.2-36.1	FGR	12	2	0.17	Brain	CR 54:1397
36.2-36.1	FGR	7	0	0	Brain	CR 54:1397
36.2-36.1	FGR	4	2	0.5	Endocrine	CR 52:770
36.2-36.1	FGR	14	6	0.43	Ovary	BJC 75:1105

Chromosome 1 - p Arm

Unknown	D1S63	39	4	0.1	Testis	CR 54:6265
Unknown	D1S247	2	1	0.5	Neuroblastom	GCC 10:275
36.2-34	D1S95-96	74	20	0.27	Breast	CR 53:1990
Unknown	D1S96	17	11	0.65	Colon	CR 50:7232
36.2-36.12	D1S95	19	2	0.11	Neuroblastom	0 7:1185
Unknown	D1S96	18	0	0	Neuroblastom	0 7:1185
32	D1S7	105	43	0.41	Breast	CR 54:4274
32	D1S7	46	13	0.28	Breast	GCC 10:275
32	D1S7	28	26	0.93	Colon	CR 50:7232
32	D1S7	14	7	0.5	Endocrine	N 328:524
32	D1S7	13	1	0.08	Liver	BJC 64:1083
32	D1S7	50	15	0.3	Liver	JJCR 37:189
32	D1S7	6	6	1	Neuroblastom	CR 55:5366
32	D1S7	14	5	0.36	Pancreas	BJC 65:100
32	D1S7	31	3	0.1	Stomach	HG 92:244
32	D1S7	45	14	0.31	Stomach	CR 51:2926
32	D1S7	31	3	0.1	Stomach	BJC 73:424
32	D1S7	30	1	0.03	Testis	GCC 10:275
Unknown	D1S233	19	5	0.26	Head&Neck	CR 54:1152
Unknown	D1S233	4	2	0.5	Neuroblastom	GCC 10:275
Unknown	D1S241	4	3	0.75	Neuroblastom	GCC 10:275
Unknown	D1S201	35	0	0	Head&Neck	CR 54:4756
Unknown	D1S201	19	1	0.05	Head&Neck	CR 54:4756
Unknown	D1S201	8	3	0.38	Neuroblastom	GCC 10:275
Unknown	D1S201	12	3	0.25	Stomach	BJC 73:424
35-32	D1S57	15	1	0.07	Brain	CR 50:5784
32	D1S57	26	12	0.46	Brain	AJP 1145:117
35-32	D1S57	11	0	0	Brain	CR 469:6572
35-32	D1S57	18	1	0.06	Breast	GCC 2:191
35-32	D1S57	73	15	0.21	Breast	GCC 10:275
35-32	D1S57	43	4	0.09	Breast	CR 50:7184
35-32	D1S57	81	36	0.44	Breast	CR 50:7271
35-32	D1S57	3	2	0.67	Breast	CR 53:3804
35-32	D1S57	44	6	0.14	Breast	CR 51:6194
35-32	D1S57	19	6	0.32	Breast	CR 51:6194
35-32	D1S57	23	5	0.22	Breast	GCC 10:275
32	D1S57	74	23	0.31	Breast	CR 53:1990
32	D1S57	52	1	0.02	Cervix	CR 54:1181
35-32	D1S57	6	0	0	Cervix	GCC 9:119
35-32	D1S57	180	40	0.22	Colon	BJC 61:475
35-32	D1S57	22	2	0.09	Colon	CCG 48:167

Chromosome 1 - p Arm

35-32	D1S57	16	6	0.38	Colon	CR 54:210
35-32	D1S57	12	0	0	Colon	N 331:273
32	D1S57	16	1	0.06	Endocrine	CR 54:270
32	D1S57	12	8	0.67	Endocrine	CR 52:770
35-32	D1S57	15	6	0.4	Endocrine	CR 54:270
32	D1S57	27	8	0.3	Esophageal	CR 54:2996
32	D1S57	14	1	0.07	Kidney	CR 54:270
35-32	D1S57	22	1	0.05	Liver	CR 51:89
35-32	D1S57	28	5	0.18	Lung	CR 54:270
32	D1S57	2	2	1	Neuroblastom	CR 55:5366
32	D1S57	14	1	0.07	Ovary	CR 54:270
35-32	D1S57	18	7	0.39	Ovary	O 7:1059
35-32	D1S57	4	0	0	Pancreas	CR 54:270
35-32	D1S57	20	2	0.1	Sarcoma	CR 52:2419
32	D1S57	5	3	0.6	Stomach	CR 54:270
35-32	D1S57	17	0	0	Testis	G 5:134
32	D1S57	12	2	0.05	Testis	CR 54:270
32	D1S57	37	2	0.05	Testis	CR 54:6265
35-32	D1S57	8	2	0.25	Uterus	CR 54:270
32	D1S57	11	1	0.09	Uterus	CR 51:5632
Unknown	D1S255	14	7	0.6	Neuroblastom	CR 54:270
Unknown	D1S255	5	4	0.8	Stomach	BJC 73:424
Unknown	D1S186	25	7	0.28	Liver	CR 54:270
32	MYCL1	74	26	0.35	Breast	CR 53:1990
32	MYCL1	81	36	0.44	Breast	CR 54:270
32	MYCL1	152	55	0.36	Breast	HG 85:101
32	MYCL1	59	23	0.39	Breast	CR 54:270
32	MYCL1	17	2	0.12	Breast	AJHG 45:73
32	MYCL1	16	10	0.62	Colon	CR 54:270
32	MYCL1	20	2	0.1	Colon	CR 52:285
32	MYCL1	20	5	0.25	Colon	CR 54:270
32	MYCL1	9	1	0.11	Endocrine	CR 52:770
32	MYCL1	20	4	0.2	Endocrine	CR 54:270
32	MYCL1	12	8	0.67	Endocrine	CR 52:770
32	MYCL1	11	0	0	Esophageal	CR 54:270
32	MYCL1	18	2	0.11	Liver	JJCR 81:108
32	MYCL1	27	0	0	Liver	CR 54:270
32	MYCL1	5	0	0	Lung	CR 54:5643
32	MYCL1	12	1	0.09	Lung	CR 54:5643
32	MYCL1	57	12	0.21	Lung	CR 54:5643
32	MYCL1	20	2	0.1	Lung	CR 54:5643
32	MYCL1	2	1	0.5	Lung	CR 54:5643
Unknown	MYCL1	9	2	0.22	Neuroblastom	CR 54:5643
32	MYCL1	41	9	0.22	Ovary	BJC 75:1105

Chromosome 1 - p Arm

32	MYCL1	13	4	0.31	Ovary	GO 55:245
32	MYCL1	17	4	0.24	Ovary	GO 55:245
32	MYCL1	27	3	0.11	Ovary	GO 55:245
32	MYCL1	9	0	0	Sarcoma	CR 52:2419
32	MYCL1	4	0	0	Testis	CCG 52:72
32	MYCL1	1	0	0	Testis	CCG 52:72
32	MYCL1	1	0	0	Testis	CCG 52:72
32	MYCL1	20	1	0.05	Uterus	CR 54:4294
Unknown	GRUT1	23	3	0.13	Testis	CR 54:4294
34.2-32.2	D1S190	23	3	0.13	Cervix	CR 56:197
34.2-32.2	D1S190	3	1	0.33	Neuroblastom	GCC 10:275
Unknown	D1S193	7	2	0.29	Neuroblastom	GCC 10:275
37	D1S211	42	6	0.14	Breast	CR 53:1990
Unknown	D1S211	5	3	0.6	Neuroblastom	GCC 10:275
Unknown	D1S197	12	7	0.58	Neuroblastom	GCC 10:275
Unknown	D1S197	16	5	0.31	Stomach	BJC 73:424
32	D1S62	74	19	0.26	Breast	CR 53:1990
32	D1S62	15	0	0	Colon	CCG 48:167
32	D1S62	2	2	1	Stomach	BJC 73:424
Unknown	D1S162	0	5	0	Breast	Unknown
Unknown	D1S162	19	5	0.26	Liver	CR 54:4188
Unknown	D1S200	12	7	0.58	Neuroblastom	GCC 10:275
Unknown	D1S200	33	5	0.15	Neuroblastom	CR 55:5681
Unknown	D1S15	74	22	0.3	Breast	CR 53:1990
Unknown	D1S15	4	1	0.25	Endocrine	CR 52:770
Unknown	D1S15	24	6	0.25	Testis	CR 54:6266
pter-22	D1S21	18	9	0.5	Brain	AJP 1145:117
pter-22	D1S21	74	20	0.27	Breast	CR 53:1990
31-pter	D1S21	10	0	0	Breast	CR 53:1990
31-pter	D1S21	12	1	0.08	Endocrine	CR 52:770
31-pter	D1S21	1	3	0.13	Endocrine	CR 52:770
31-pter	D1S17	19	8	0.42	Brain	AJP 1145:117
31-pter	D1S17	8	1	0.12	Breast	CR 53:1990
31-pter	D1S17	5	0	0	Breast	CR 51:1020
pter-22	D1S17	73	27	0.5	Breast	CR 53:1990
pter-22	D1S17	4	3	0.75	Endocrine	CR 52:770
pter-22	D1S17	9	2	0.27	Endocrine	CR 52:770
31-pter	D1S17	13	2	0.15	Endocrine	GCC 13:9
pter-22	D1S17	19	4	0.21	Melanoma	CR 53:1990
pter-22	D1S18	74	20	0.27	Breast	CR 53:1990
pter-22	D1S18	6	4	0.67	Endocrine	CR 52:770

Chromosome 1 - p Arm

Unknown	D1S203	14	6	0.43	Neuroblastom	GCC 10:275 a
Unknown	D1S246	11	0	0	Stomach	BJC 74:421
Unknown	D1S209	15	7	0.47	Neuroblastom	GCC 10:275 a
Unknown	D1S159	16	3	0.19	Liver	CR 54:4188
Unknown	D1S219	8	0	0	Stomach	BJC 73:424
31	D1S461	44	11	0.25	Breast	CR 53:1990
21	D1S216	14	13	0.93	Neuroblastom	CR 55:5366 a
21	D1S216	8	4	0.5	Neuroblastom	GCC 10:275 a
pter-31	D1S2	12	7	0.58	Brain	AJP 145:1175
pter-31	D1S2	1	0	0	Breast	GCC 12:16
pter-31	D1S2	74	19	0.26	Breast	CR 53:1990
pter-31	D1S2	16	3	0.19	Melanoma	PNAS 86:4614
31	D1S500	33	8	0.24	Breast	CR 55:1752
31	D1S480	39	11	0.28	Breast	CR 55:1752
Unknown	D1S207	15	8	0.53	Neuroblastom	GCC 10:275 a
Unknown	D1S207	14	2	0.14	Stomach	BJC 74:421
pter-22	D1S16	74	22	0.3	Breast	CR 53:1990
pter-22	D1S16	11	0	0	Cervix	CR 54:4188
pter-22	D1S16	6	2	0.33	Endocrine	CR 52:770
pter-22	D1S16	24	4	0.17	Melanoma	PNAS 86:4614
pter-22	D1S16	13	5	0.38	Testis	CR 54:6266
31	D1S225	36	7	0.19	Breast	CR 55:1752
Unknown	D1S167	9	1	0.11	Liver	CR 54:4188
Unknown	AF3	10	0	0	Breast	AJHG 115:73
Unknown	AF3	26	6	0.23	Testis	CR 54:6265
Unknown	D1S236	11	5	0.45	Neuroblastom	GCC 10:275 a
22-13	D1S10	74	19	0.26	Breast	CR 53:1990
Unknown	AMY2A	17	0	0	Testis	CR 54:6265
21	AMY2B	16	5	0.31	Liver	CR 54:4188
21	AMY2B	16	3	0.15	Ovary	CR 54:4188
21	AMY2B	12	0	0	Uterus	CR 54:4294
22-13	D1S14	74	20	0.32	Breast	CR 53:1990
22-13	D1S14	18	3	0.17	Endocrine	GCC 13:9
22-13	D1S14	23	4	0.17	Testis	CR 54:6265
21-13	D1S73	13	6	0.46	Brain	AJP 145:1175
21-13	D1S73	74	23	0.31	Breast	CR 53:1990
21-13	D1S73	22	6	0.27	Breast	GCC 12:16
21-13	D1S73	23	6	0.26	Testis	CR 54:6265
22-13	D1S9	8	6	0.75	Brain	AJP 145:1175
22-13	D1S9	74	23	0.31	Breast	CR 53:1990
22-13	D1S9	25	0	0	Testis	CR 54:6265
12	RAP1A	18	1	0.06	Colon	CR 54:4188

Chromosome 1 - p Arm

13	DIS418	39	8	0.21	Breast	CR 55:1752
13	NRAS	74	21	0.28	Breast	CR 53:1990
13	NRAS	10	5	0.5	Endocrine	CR 52:770
13	NRAS	6	1	0.17	Endocrine	CR 52:770
13	NGFB	32	13	0.41	Brain	AJP 145:1175
13	NGFB	6	0	0	Breast	CCG 52:72
13	NGFB	13	2	0.15	Breast	AJHG 45:73
13	NGFB	13	9	0.69	Breast	CR 53:1990
13	NGFB	18	3	0.17	Colon	IJC 53:382
13	NGFB	5	1	0.2	Testis	CCG 52:72
13	NGFB	16	0	0	Testis	CR 54:6266
13	NGFB	1	0	0	Testis	CCG 52:72
13	NGFB	3	0	0	Testis	CCG 52:72
13	NGFB	6	0	0	Uterus	CR 53:1990
22-13	DIS11	74	19	0.26	Breast	CR 53:1990
21-Nov	DIS36	17	2	0.12	Breast	CR 53:1990
22-13	DIS13	74	16	0.22	Breast	CR 53:1990
22-13	DIS13	7	6	0.86	Endocrine	CR 52:770
22-13	DIS13	7	6	0.86	Endocrine	CR 52:770
22-13	DIS64	18	10	0.56	Brain	JNCI 84:506
31-pter	Unknown	36	1	0.03	Breast	CR 53:1990
32	DIS100-101	74	20	0.27	Breast	CR 53:1990
Unknown	DIS33	9	4	0.44	Breast	CR 51:1020
3-35-5	Unknown	37	6	0.16	Colon	BMC 98:150
Unknown	Unknown	14	0	0	Colon	CCG 48:167
Unknown	DIS188	23	1	0.17	Endocrine	CCG 52:72
Unknown	DIS19	4	2	0.5	Endocrine	CR 52:770
Unknown	PND	3	2	0.67	Endocrine	CR 52:770
Unknown	DIS252	19	3	0.16	Head&Neck	CR 54:1152
Unknown	DIS57-NGFB	21	4	0.19	Head&Neck	CR 52:770
Unknown	DIS243-DIS228	22	1	0.05	Kidney	PNAS 92:2854
Unknown	DIS243-DIS228	6	0	0	Kidney	PNAS 92:2854
Unknown	DIS:243-228	33	3	0.09	Kidney	CR 55:6189
33-35	Unknown	14	2	0.14	Liver	CR 54:4188
Unknown	DIS187	19	4	0.21	Liver	CR 54:4188
Unknown	ISO1	27	6	0.22	Liver	CR 54:4188
Unknown	ISO2	13	4	0.31	Liver	CR 54:4188
Unknown	DIS19	21	6	0.29	Melanoma	PNAS 92:2854
Unknown	DIS:214-201-255	20	1	0.05	Melanoma	CR 56:589
Unknown	PND	13	3	0.36	Melanoma	PNAS 92:2854
Unknown	DIS220	20	10	0.5	Neuroblastom	GCC 10:275
Unknown	DIS232	11	1	0.61	Neuroblastom	GCC 10:275
Unknown	DIS252	8	2	0.25	Neuroblastom	GCC 10:275

Chromosome 1 - p Arm

Unknown	D1S97	18	0	0	Neuroblastom	0 7:1185
Unknown	GGAT2A07	28	3	0.11	Neuroblastom	CR 55:5681
Unknown	D1S80	18	1	0.06	Ovary	UC 54:546
Unknown	D1S:162-175	14	1	0.07	Ovary	BJC 72:1330
Unknown	FE-AMY	25	6	0.24	Ovary	CF 53:2393
Unknown	MTHFR	28	16	0.57	Ovary	BJC 75:1105
13-36	PND-D1S2-NGEB	11	0	0	Prostate	GND:530
3.3-.5	Unknown	9	3	0.33	Stomach	BJC 59:750
SOM		7135	1886	0.26		

Chromosome 1 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D1S305	30	7	0.23	Cervix	CR 55:199
CENTR	D1S305	14	1	0.07	Neuroblastoma	CR 55:5366
Unknown	D1S67	30	1	0.03	Brain	AJP 145:1175
21	D1S67	74	7	0.09	Breast	CR 53:1990
Unknown	D1S67	15	2	0.13	Breast	CR 50:2184
Unknown	D1S67	7	2	0.29	Cervix	GCC 9:119
Unknown	D1S67	26	3	0.12	Esophageal	GCC 13:249
Unknown	D1S67	14	1	0.07	Kidney	CR 51:820
Unknown	D1S67	6	1	0.17	Lung	CR 52:2478
Unknown	D1S67	3	3	1	Lung	CR 52:2478
Unknown	D1S67	1	1	1	Lung	CR 52:2478
Unknown	D1S67	17	5	0.29	Lung	CR 52:2478
Unknown	D1S67	14	4	0.29	Ovary	CR 51:4118
21	D1S67	23	2	0.09	Ovary	IJC 54:546
Unknown	D1S67	26	3	0.12	Testis	CR 51:5265
Unknown	D1S67	22	4	0.18	Uterus	GCC 9:119
21-23	MUC1	74	9	0.12	Breast	CR 53:1990
21-23	MUC1	7	0	0	Breast	CR 53:3804
21-23	MUC1	44	13	0.3	Breast	GCC 12:16
21-23	MUC1	43	7	0.16	Breast	CR 51:1020
21-23	MUC1	21	7	0.33	Head&Neck	CR 52:1494
21-23	MUC1	16	4	0.25	Stomach	CR 51:2926
21-23	MUC1	25	2	0.08	Testis	GCC 13:249
21	PEM-pMUC10	89	14	0.16	Breast	GCC 5:311
21	SPTA1	74	9	0.12	Breast	CR 53:1990
21	SPTA1	6	2	0.33	Breast	GCC 12:16
21	SPTA1	6	2	0.33	Breast	PN 86:7204
21	SPTA1	22	2	0.09	Colon	CR 52:285
21	SPTA1	29	3	0.1	Colon	CR 52:285
Unknown	D1S176	17	1	0.06	Liver	CR 54:4188
22-25	ATP1B1	74	9	0.12	Breast	CR 53:1990
21-23	APOA2	6	0	0	Breast	GCC 2:191
21-23	APOA2	18	4	0.22	Ovary	INTJ 65:229
21-23	APOA2	5	0	0	Testis	GCC 13:249
21-23	APOA2	26	2	0.08	Uterus	CR 51:4118
21-31	D1S61	74	10	0.14	Breast	CR 53:1990
21-31	D1S61	52	12	0.23	Breast	CR 51:1020
21-31	D1S61	39	8	0.21	Breast	GCC 12:16
21-31	D1S61	21	2	0.1	Endocrine	GCC 13:249
Unknown	D1S75	14	0	0	Brain	AJP 145:1175
Unknown	D1S75	18	1	0.06	Testis	CR 51:5265
Unknown	D1S66	14	4	0.29	Esophageal	CR 54:2996
Unknown	D1S66	11	0	0	Sarcoma	CR 52:2419
23-25	AT3	19	0	0	Brain	CR 54:1397
23-25	AT3	14	0	0	Brain	CR 54:1397

Chromosome 1 - q Arm

23-25	AT3	14	1	0.07	Breast	AJHG 45:73
23-25	AT3	2	0	0	Breast	GCC 24:191
23-25	AT3	14	0	0	Colon	CR 52:285
23-25	AT3	1	0	0	Liver	GCC 48:72
23-25	AT3	22	1	0.05	Ovary	IJC 54:546
23-25.1	AT3	5	0	0	Ovary	CR 54:6265
23-25	AT3	27	0	0	Testis	CR 54:6265
23-25	AT3	8	2	0.25	Testis	GCC 43:249
Unknown	D1S238	22	4	0.18	Cervix	CR 56:197
31-32.1	F13B	9	0	0	Brain	CR 54:1397
31-32.1	F13B	15	0	0	Brain	CR 54:1397
31-32.1	F13B	12	1	0.08	Endocrine	GCC 45:9
31-32.1	F13B	13	0	0	Uterus	CR 54:4294
Unknown	D1S65	18	0	0	Brain	AJP 145:1175
Unknown	D1S65	18	5	0.28	Breast	GCC 12:16
Unknown	D1S65	6	0	0	Esophageal	CR 51:2113
Unknown	D1S65	16	2	0.12	Head&Neck	CR 52:1494
Unknown	D1S65	15	3	0.2	Testis	CR 54:6265
32 or 42	REN	11	0	0	Brain	AJP 145:1175
32 or 42	REN	12	3	0.25	Breast	CR 51:1020
32	REN	21	7	0.33	Breast	GCC 12:16
32 or 42	REN	6	1	0.17	Breast	CR 53:990
32 or 42	REN	12	2	0.17	Cervix	CR 49:3598
32	REN	16	1	0.06	Colon	CR 52:285
32 or 42	REN	19	7	0.37	Colon	IJC 53:382
32 or 42	REN	8	0	0	Liver	PNAS 86:8852
32 or 42	REN	14	0	0	Liver	JJCR 81:108
32 or 42	REN	4	0	0	Neuroblastom	CR 49:1095
32 or 42	REN	21	1	0.05	Ovary	IJC 54:546
32 or 42	REN	8	0	0	Prostate	GCC 47:130
32 or 42	REN	15	4	0.27	Stomach	CR 52:3099
32 or 42	REN	11	3	0.27	Testis	CR 54:6265
32 or 42	REN	6	0	0	Uterus	CR 51:5632
32	D1S249	12	0	0	Neuroblastom	CR 51:5636
Unknown	LAMB2	13	1	0.08	Testis	CR 54:6265
Unknown	D1S58	24	0	0.46	Breast	GCC 47:130
Unknown	D1S58	27	7	0.26	Cervix	CR 54:4481
Unknown	D1S58	15	0	0	Colon	GCC 48:72
Unknown	D1S58	21	4	0.19	Testis	CR 54:6265
Unknown	D1S58	23	5	0.22	Testis	CR 54:6265
Unknown	D1S81	32	0	0	Brain	AJP 145:1175
Unknown	D1S81	39	12	0.31	Breast	GCC 12:16
Unknown	D1S81	41	5	0.12	Breast	CR 53:4356
Unknown	D1S81	20	1	0.05	Liver	CR 51:89
Unknown	D1S213	30	6	0.2	Cervix	CR 56:197

Chromosome 1 - q Arm

Unknown	D1S251	51	4	0.04	Kidney	CR 54:4481
Unknown	D1S74	11	4	0.36	Breast	GCC 12:16
Unknown	D1S8	51	15	0.29	Breast	GCC 12:16
Unknown	D1S74	39	7	0.18	Cervix	CR 54:4481
Unknown	D1S8	9	0	0	Endocrine	CR 54:4481
32-44	D1S103	18	2	0.11	Ovary	BJC 69:429
Unknown	D1S74	4	0	0	Testis	CR 54:4481
Unknown	D1S74	50	3	0.06	Testis	CR 54:3983
Unknown	D1S74	54	3	0.06	Testis	CR 54:3983
Unknown	D1S8	31	2	0.06	Testis	GCC 13:249
Unknown	D1S8	31	2	0.06	Testis	GCC 13:249
21-23	Unknown	70	18	0.26	Breast	JNCI 84:506
21-24	Unknown	75	16	0.21	Breast	JNCI 84:506
Unknown	DF3	43	6	0.14	Breast	IJC 61:1
4.2-.3	Unknown	34	4	0.12	Colon	BJC 59:750
2.1-.4	Unknown	27	3	0.11	Colon	BJC 59:750
Unknown	D1S102	12	1	0.03	Endocrine	GCC 12:16
Unknown	D1S215	11	2	0.18	Endocrine	CR 56:599
Unknown	D1S259	22	5	0.23	Head&Neck	CR 54:4756
Unknown	D1S304-212	43	6	0.14	Head&Neck	CR 54:4756
Unknown	D1S304-212	17	2	0.12	Head&Neck	CR 54:4756
Unknown	Unknown	8	3	0.38	Liver	BJC 64:1083
42-43	Unknown	13	3	0.23	Liver	BJC 64:1083
Unknown	Unknown	4	1	0.25	Liver	BJC 64:1083
Unknown	D1S:237-212	27	2	0.07	Melanoma	CR 56:589
Unknown	APOA2-D1S:158-103	14	0	0	Ovary	BJC 72:1330
Unknown	REN-D1981	23	9	0.39	Ovary	CR 54:2393
Unknown	Unknown	13	2	0.15	Pancreas	BJC 65:809
32-44	Unknown	7	0	0	Pancreas	CR 54:2761
4.2-.3	Unknown	6	1	0.17	Stomach	BJC 59:750
2.1-.4	Unknown	10	5	0.5	Stomach	BJC 59:750
Unknown	AGT	52	3	0.06	Testis	CR 54:3983
Unknown	AGT	4	0	0	Testis	CR 54:3983
Unknown	CR2	21	3	0.14	Testis	CR 54:6265
Unknown	D1S180	3	0	0	Testis	CR 54:3983
Unknown	D1S180	50	7	0.14	Testis	CR 54:3983
Unknown	D1S235	2	0	0	Testis	CR 54:3983
Unknown	D1S235	39	4	0.1	Testis	CR 54:3983
STUD		2869	417	0.15		

Chromosome 2 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D2S44	7	1	0.14	Uterus	GCC 9:119
Unknown	Unknown	11	1	0.09	Brain	CR 50:5784
Unknown	D2S44	7	1	0.14	Breast	CR 53:3804
Unknown	D2S44	74	6	0.08	Breast	CR 53:4356
Unknown	D2S47	23	0	0	Breast	CR 50:7184
23-15	D2S6	27	3	0.11	Breast	GCC 2:191
23-15	D2S6	22	2	0.09	Breast	JNCI 84:506
23-15	D2S6	42	5	0.12	Breast	CR 53:4356
23-PTER	TPO	50	21	0.42	Breast	BCRT 32:5
Unknown	D2S139	27	4	0.15	Cervix	CR 56:197
Unknown	D2S177	18	2	0.11	Cervix	CR 56:197
Unknown	D2S44	7	0	0	Cervix	GCC 9:119
Unknown	D2S44	48	6	0.12	Cervix	CR 54:4481
Unknown	D2S48	26	3	0.12	Cervix	CR 54:4481
Unknown	APOB	7	0	0	Colon	CCG 48:167
Unknown	D2S44	236	37	0.16	Colon	BJC 64:475
Unknown	D2S45	14	0	0	Colon	CCG 48:167
Unknown	D2S155	11	2	0.18	Endocrine	CR 56:599
Unknown	D2S44	60	10	0.17	Esophageal	GCC 10:177
Unknown	D2S44	20	4	0.2	Esophageal	CR 54:2996
Unknown	D2S47	41	10	0.24	Esophageal	GCC 10:177
Unknown	D2S47	30	2	0.07	Esophageal	CR 54:2996
Unknown	D2S162	21	4	0.19	Head&Neck	CR 54:1152
Unknown	D2S166-149	15	0	0	Head&Neck	CR 54:4756
Unknown	D2S166-149	20	1	0.05	Head&Neck	CR 54:4756
Unknown	D2S207-D2S131	21	0	0	Kidney	PNAS 92:2854
Unknown	D2S207-D2S131	6	0	0	Kidney	PNAS 92:2854
Unknown	D2S47	11	2	0.18	Kidney	CR 51:820
Unknown	D2S207-131	32	0	0	Kidney	CR 55:6189
Unknown	D2S48	9	0	0	Liver	CR 51:89
13	TGFA	5	0	0	Liver	PNAS 86:8852
Unknown	Unknown	27	6	0.22	Lung	CR 54:2322
Unknown	D2S44	7	2	0.29	Lung	CR 54:5643
Unknown	D2S44	4	2	0.5	Lung	CR 54:5643
Unknown	D2S44	22	11	0.5	Lung	CR 54:5643
Unknown	D2S47	19	1	0.05	Lung	CR 52:2478
12	CD8A	20	3	0.15	Ovary	BJC 69:429
Unknown	D2S44	23	9	0.39	Ovary	CR 53:2393
Unknown	D2S47	11	0	0	Ovary	CR 51:5118
23-15	D2S6	31	7	0.23	Ovary	IJC 54:546
23-PTER	TPO	14	2	0.14	Ovary	BJC 69:429
Unknown	D2S1	14	1	0.07	Prostate	G 11:530
Unknown	D2S3-D2S6	6	0	0	Prostate	G 11:530
Unknown	D2S47	10	2	0.2	Sarcoma	CR 52:2419
Unknown	D2S123	13	1	0.08	Stomach	CR 55:1933
Unknown	D2S44	45	12	0.27	Testis	O 9:2245

Chromosome 2 - p Arm

Unknown	D2S48	31	5	0.16	Testis	O 9:2245
24	MYCN	2	0	0	Testis	CCG 52:72
24	MYCN	2	0	0	Testis	CCG 52:72
24	MYCN	2	0	0	Testis	CCG 52:72
13	D2S101	21	0	0	Uterus	CR 54:4294
Unknown	D2S44	7	1	0.14	Uterus	GCC 9:119
SUM		1272	191	0.15		

Chromosome 2 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
13	TL1A	20	0	0	Uterus	CR 54:4294
Unknown	D2S44	17	0	0	Brain	CR 49:6572
Unknown	D2S44	17	0	0	Brain	CR 50:5784
Unknown	CRYG	8	1	0.12	Breast	GCC 2:191
Unknown	D2S44	51	7	0.14	Breast	GCC 4:113
Unknown	D2S44	31	3	0.1	Breast	GCC 2:191
Unknown	D2S44	49	5	0.1	Breast	CR 50:7184
Unknown	CRYG	9	1	0.11	Cervix	CR 49:3598
Unknown	D2S122	28	4	0.14	Cervix	CR 56:197
Unknown	D2S172	29	7	0.24	Cervix	CR 56:197
Unknown	CRYG	21	0	0	Colon	N 331:273
35-37	D2S3	16	0	0	Colon	CCG 48:167
Unknown	D2S44	32	1	0.03	Colon	CCG 48:167
Unknown	D2S54	8	0	0	Colon	CCG 48:167
Unknown	D2S125	20	2	0.1	Endocrine	CR 56:599
Unknown	D2S44	14	1	0.07	Esophageal	CR 51:2113
Unknown	D2S55	13	0	0	Esophageal	CR 54:3996
Unknown	D2S111	20	3	0.15	Head&Neck	CR 54:1152
Unknown	D2S163	10	0	0	Head&Neck	CR 54:4756
Unknown	D2S163	20	4	0.2	Head&Neck	CR 54:4756
Unknown	D2S125	28	1	0.04	Kidney	PNAS 92:2854
Unknown	D2S44	38	5	0.13	Kidney	CR 51:820
33-35	CRYP1	1	0	0	Liver	CR 51:89
Unknown	D2S44	18	0	0	Liver	CR 51:89
Unknown	D2S44	4	0	0	Liver	PNAS 86:8852
p16-15	D2S5	4	0	0	Liver	CCG 48:72
Unknown	D2S44	40	11	0.28	Lung	CR 52:478
p16-15	D2S5	1	0	0	Neuroblastoma	CR 49:1095
Unknown	D2S3	23	9	0.39	Ovary	CR 53:2393
Unknown	D2S44	29	4	0.14	Ovary	CR 51:5118
p16-15	D2S5	5	1	0.2	Ovary	CR 50:2724
Unknown	D2S50	10	0	0	Ovary	CR 50:2724
Unknown	D2S55	19	2	0.11	Ovary	IJC 54:546
Unknown	D2S72	16	6	0.38	Ovary	BJC 69:429
Unknown	D2S44	4	0	0	Pancreas	CR 54:2761
Unknown	D2S44	26	7	0.27	Sarcoma	CR 52:2419
Unknown	D2S44	18	1	0.06	Stomach	HG 92:244
Unknown	D2S44	27	0	0	Testis	LI 73:606
13	TL1A	20	0	0	Uterus	CR 54:4294
SUM		744	86	0.12		

Chromosome 3 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
26	D3S17	12	10	0.83	Kidney	CR 51:1071
26	D3S17	7	7	1	Lung	GCC 1:240
Unknown	D3S1307	36	2	0.06	Esophageal	BJC 73:366
Unknown	D3S1317	31	10	0.32	Kidney	BJC 69:230
Unknown	D3S1317	12	3	0.25	Stomach	CR 55:1933
25	D3S18	19	9	0.47	Kidney	CR 51:1071
25	D3S18	1	1	1	Lung	GCC 1:240
14	D3S1038	21	6	0.29	Esophageal	CR 54:6484
14	D3S1038	37	5	0.14	Esophageal	BJC 73:366
14	D3S1038	5	0	0	Kidney	GCC 12:76
14	D3S1038	40	19	0.47	Kidney	BJC 69:230
14	D3S1038	6	5	0.83	Lung	JAMA 273:55
14	D3S1038	1	1	1	Lung	JAMA 273:55
14	D3S1038	25	3	0.12	Uterus	CR 54:4294
Unknown	D3S1263	22	7	0.32	Cervix	CR 56:197
Unknown	D3S651	6	4	0.67	Kidney	CR 51:4707
Unknown	D3S651	18	3	0.17	Lung	CR 52:873
Unknown	D3S651	8	8	1	Lung	CR 52:873
24-25	RAF1	4	1	0.25	Breast	CR 53:3804
24-25	RAF1	3	1	0.33	Cervix	CR 49:3598
25	RAF1	10	10	1	Head&Neck	CGC 54:91
25	RAF1	1	0	0	Kidney	CR 51:4707
25	RAF1	22	20	0.91	Kidney	CR 51:1071
25	RAF1	12	9	0.75	Kidney	CR 51:1544
25	RAF1	2	2	1	Kidney	CR 51:1071
25	RAF1	22	10	0.45	Kidney	G 11:537
24-25	RAF1	17	9	0.53	Kidney	CR 49:1390
24-25	RAF1	4	2	0.5	Lung	GCC 1:95
24-25	RAF1	15	14	0.93	Lung	GCC 1:95
25	RAF1	1	1	1	Lung	CR 49:5130
24-25	RAF1	1	0	0	Lung	GCC 1:95
25	RAF1	5	5	1	Lung	O 4:451
25	RAF1	12	2	0.17	Prostate	G 11:530
25	RAF1	1	1	1	Uterus	CR 51:5632
24-25	D3S1286	37	12	0.32	Esophageal	BJC 69:1
Unknown	D3S1293	33	5	0.15	Esophageal	BJC 73:366
Unknown	D3S1293	40	2	0.05	Head&Neck	CR 54:4756
Unknown	D3S1293	39	10	0.26	Head&Neck	CR 54:4756
Unknown	D3S1020	5	5	1	Lung	CR 52:873
Unknown	D3S1020	7	3	0.43	Lung	CR 52:873
Unknown	D3S1002	5	5	1	Lung	CR 52:873
Unknown	D3S1002	12	3	0.25	Lung	CR 52:873
25.1	D3S669	22	3	0.14	Breast	CR 51:5794
25.1	D3S669	10	7	0.7	Kidney	CR 51:4707
Unknown	D3S669	5	5	1	Lung	CR 52:873
Unknown	D3S669	12	2	0.17	Lung	CR 52:873

Chromosome 3 - p Arm

Unknown	THRB	54	15	0.28	Breast	GCC 12:129
21-PTER	THRB	30	4	0.13	Breast	AJP 140:215
22-24.1	THRB	71	32	0.45	Breast	CR 54:3021
Unknown	THRB	24	9	0.38	Cervix	IJC 58:787
22-24.1	THRB	7	3	0.43	Cervix	CR 49:3598
24	THRB	9	1	0.11	Colon	IJC 53:382
24	THRB	44	10	0.23	Esophageal	BJC 73:366
24	THRB	9	3	0.33	Head&Neck	C 72:881
22-24.1	THRB	23	6	0.26	Head&Neck	CR 54:1152
22-24.1	THRB	3	0	0	Head&Neck	CGC 54:91
22-24.1	THRB	5	5	1	Kidney	CR 51:949
24	THRB	34	18	0.53	Kidney	G 11:537
22-24.1	THRB	11	11	1	Lung	CR 49:5130
21-PTER	THRB	1	0	0	Lung	GCC 1:95
24	THRB	7	3	0.43	Lung	GCC 1:958
22-24.1	THRB	2	2	1	Lung	GCC 1:95
22-24.1	THRB	3	1	0.33	Lung	GCC 1:95
22-24.1	THRB	5	3	0.6	Lung	GCC 1:95
24	THRB	6	5	0.83	Lung	O 4:451
22-24.1	THRB	10	2	0.2	Lung	GCC 11:15
22-24.1	THRB	22	17	0.77	Lung	GCC 1:95
Unknown	THRB	38	22	0.58	Melanoma	GCC 15:102
24	THRB	22	5	0.23	Ovary	IJC 52:575
22-24.1	THRB	7	4	0.57	Ovary	O 5:219
Unknown	THRB	22	6	0.27	Ovary	IJC 54:546
22-24.1	THRB	17	5	0.29	Ovary	BJC 69:429
Unknown	THRB	16	0	0	Pediatric	CR 50:3279
24	THRB	11	0	0	Prostate	GCC 11:119
Unknown	THRB	2	0	0	Uterus	CR 51:5632
24	THRB	4	1	0.25	Uterus	CR 51:5632
24	THRB	5	3	0.6	Kidney	G 11:537
24.2-25	D3S1266	52	15	0.29	Esophageal	IJC 69:1
23	D3S647	24	2	0.08	Breast	CR 51:5794
23	D3S647	21	8	0.38	Esophageal	CR 54:6484
23	D3S647	30	4	0.13	Esophageal	BJC 73:366
23	D3S647	22	8	0.36	Kidney	BJC 69:230
23	D3S647	11	5	0.45	Kidney	CR 51:4707
pter-21	D3S12	5	0	0	Stomach	HG 89:445
22-24.2	D3S1211	17	4	0.24	Esophageal	IJC 69:1
21.3	D3S1029	23	4	0.17	Esophageal	CR 54:6484
21.3	D3S1029	1	1	1	Lung	JAMA 273:55
21.3	D3S1029	6	5	0.83	Lung	JAMA 273:55
Unknown	D3S867	18	5	0.28	Lung	CR 52:873
Unknown	D3S867	7	7	1	Lung	CR 52:873
Unknown	D3S1298	24	8	0.33	Cervix	CR 56:197
13	D3S685	54	6	0.11	Breast	CR 51:5794

Chromosome 3 - p Arm

Unknown	D3S685	6	3	0.5	Cervix	GCC 9:119
21.3-22	D3S1007	17	9	0.53	Esophageal	CR 54:6484
21.3-22	D3S1007	33	6	0.18	Esophageal	BJC 73:366
Unknown	D3S685	47	15	0.32	Esophageal	GCC 10:177
21.3-22	D3S1007	3	0	0	Kidney	GCC 12:76
Unknown	D3S685	27	18	0.67	Kidney	CR 51:4707
21.3-22	D3S1007	50	37	0.74	Lung	IJC 64:373
Unknown	D3S685	31	14	0.45	Lung	CR 52:873
Unknown	D3S685	10	10	1	Lung	CR 52:873
13	D3S685	1	1	1	Lung	CR 52:2478
13	D3S685	7	7	1	Lung	CR 52:2478
13	D3S685	3	3	1	Lung	CR 52:2478
13	D3S685	26	9	0.35	Lung	CR 52:2478
13	D3S685	18	3	0.17	Ovary	CR 51:5118
Unknown	D3S685	18	3	0.17	Ovary	CR 51:5118
Unknown	D3S685	11	2	0.18	Uterus	GCC 9:119
22-24.2	D3S1260	63	25	0.4	Esophageal	IJC 69:1
22-24.2	D3S1260	3	0	0	Melanoma	GCC 15:102
21	D3S11	16	0	0	Endocrine	CR 56:599
21	D3S11	7	4	0.57	Kidney	CR 49:1390
21	D3S2-93	1	1	1	Breast	GCC 2:191
21	D3S2-S3	20	1	0.05	Breast	GCC 2:191
21	D3S2-S3	1	0	0	Breast	PN 84:2372
21	D3S2-S3	2	0	0	Breast	PN 84:2372
21	D3S2-S3	3	0	0	Breast	PN 84:2372
21.3	D3S686	34	2	0.06	Breast	CR 51:5794
21	D3S2	22	4	0.18	Cervix	CR 54:4481
Unknown	D3S2	16	6	0.38	Cervix	IJC 58:787
21	D3S2	9	9	1	Cervix	CR 49:3598
21	D3S2	16	3	0.19	Colon	IJC 53:382
21	D3S2	9	0	0	Colon	N 331:273
Unknown	D3S2	12	0	0	Endocrine	GCC 13:9
21	D3S2	22	8	0.36	Esophageal	CR 54:2996
Unknown	D3S2	10	1	0.1	Esophageal	CR 51:2113
21.3	D3S686	38	11	0.29	Esophageal	BJC 73:366
21	D3S2	4	3	0.75	Head&Neck	CGC 54:91
21	D3S2	14	6	0.43	Kidney	CR 51:949
Unknown	D3S2	2	0	0	Kidney	CR 51:1544
Unknown	D3S2	23	18	0.78	Kidney	CR 51:1071
Unknown	D3S2	2	1	0.5	Kidney	CGC 32:281
Unknown	D3S2	11	2	0.18	Kidney	PNAS 85:157
21	D3S2	14	8	0.57	Kidney	G 11:537
Unknown	D3S2	20	9	0.45	Kidney	CR 51:1544
14-21	D3S2	8	7	0.88	Kidney	CR 49:1390
21	D3S2	8	7	0.88	Kidney	N 327:721
21.3	D3S686	10	6	0.6	Kidney	CR 51:4707

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Unknown	D3S2	4	1	0.25	Leukemia	CGC 61:42
21	D3S2	15	12	0.8	Lung	PNAS 84:925
21	D3S2	1	0	0	Lung	PNAS 84:925
21	D3S2	5	1	0.2	Lung	GCC 11:15
21	D3S2	5	2	0.4	Lung	GCC 1:95
Unknown	D3S2	1	0	0	Lung	N 329:451
21	D3S2	1	0	0	Lung	PNAS 84:925
21	D3S2	7	7	1	Lung	PNAS 84:925
21	D3S2	8	6	0.75	Lung	PNAS 86:509
Unknown	D3S2	9	8	0.89	Lung	N 329:451
Unknown	D3S2	1	0	0	Lung	N 329:451
21	D3S2	6	6	1	Lung	GCC 1:240
21	D3S2	6	5	0.83	Lung	PNAS 84:925
Unknown	D3S2	20	8	0.4	Lung	JJCR 80:924
Unknown	D3S2	6	5	0.83	Lung	NEJ 317:110
Unknown	D3S2	4	3	0.75	Lung	NEJ 317:110
Unknown	D3S2	2	1	0.5	Lung	NEJ 317:110
Unknown	D3S2	12	0	0	Lung	PNAS 84:925
21	D3S2	9	4	0.44	Lung	PNAS 86:509
21	D3S2	12	8	0.67	Lung	JJCR 80:924
21	D3S2	3	1	0.33	Lung	GCC 1:95
21	D3S2	11	8	0.73	Lung	GCC 1:95
21	D3S2	8	8	1	Lung	CR 49:5130
14-21	D3S2	5	5	1	Lung	GCC 5:119
21.3	D3S686	6	6	1	Lung	CR 52:873
21.3	D3S686	11	7	0.64	Lung	CR 52:873
Unknown	D3S2	11	6	0.55	Melanoma	GCC 15:102
Unknown	D3S2	6	0	0	Neuroblastoma	CR 49:1095
21	D3S2	16	1	0.06	Ovary	IJC 54:546
21	D3S2	6	4	0.67	Sarcoma	CGC 53:45
21	D3S2	12	4	0.33	Sarcoma	CR 52:2419
Unknown	D3S2	10	0	0	Stomach	CR 48:2988
Unknown	D3S2	19	1	0.05	Testis	O 9:2245
21	D3S2	12	4	0.33	Testis	G 5:134
Unknown	D3S2	5	0	0	Uterus	CR 51:5632
14.2	D3S3	1	0	0	Breast	GCC 2:191
14.2	D3S3	9	9	1	Head&Neck	CGC 54:91
14.2	D3S3	4	3	0.75	Kidney	CR 51:1071
14.2	D3S3	1	1	1	Kidney	CR 49:1390
14.2	D3S3	9	0	0	Kidney	PNAS 85:157
14.2	D3S3	2	1	0.5	Kidney	N 327:721
14.2	D3S3	3	1	0.33	Kidney	G 11:537
14.2	D3S3	5	3	0.6	Lung	GCC 1:95
14.2	D3S3	1	1	1	Lung	GCC 1:95
14.2	D3S3	4	4	1	Lung	GCC 1:240
14.2	D3S3	1	0	0	Lung	N 329:451

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14.2	D3S3	9	6	0.67	Lung	N 329:451
14.2	D3S3	3	3	1	Lung	GCC 1:95
14.2	D3S3	1	0	0	Lung	N 329:451
14.2	D3S3	2	1	0.5	Lung	NEJ 317:110
14.2	D3S3	4	3	0.75	Lung	NEJ 317:110
14.2	D3S3	4	0	0	Lung	GCC 11:15
14.2	D3S3	1	1	1	Lung	GCC 1:95
21.2-14.2	D3S32	8	0	0	Brain	CR 49:6572
21.2-14.2	D3S32	18	2	0.11	Brain	CR 50:5784
21.2-14.2	D3S32	16	3	0.19	Breast	CR 50:7184
21.2-14.2	D3S32	44	3	0.2	Breast	CR 51:5794
21.2-14.2	D3S32	30	12	0.4	Cervix	CR 54:4481
14.2-21.2	D3S32	3	3	1	Cervix	GCC 9:119
21.2-14.2	D3S32	17	7	0.41	Cervix	IJC 58:787
14.2-21.2	D3S32	4	1	0.25	Cervix	IJC 67:71
14.2-21.2	D3S32	19	8	0.42	Esophageal	CR 54:2996
21.2-14.2	D3S32	28	10	0.36	Esophageal	BJC 73:366
21.2-14.2	D3S32	7	0	0	Head&Neck	C 72:881
21.2-14.2	D3S32	15	8	0.53	Kidney	CR 51:820
14.2-21.2	D3S32	15	9	0.6	Kidney	CR 51:4707
14.2-21.2	D3S32	21	17	0.81	Kidney	CR 51:1071
21.2-14.2	D3S32	18	8	0.44	Kidney	CR 51:949
21.2-14.2	D3S32	20	2	0.1	Liver	CR 51:89
21.2-14.2	D3S32	11	6	0.55	Lung	GCC 3:358
21.2-14.2	D3S32	17	11	0.65	Lung	CR 52:873
21.2-14.2	D3S32	6	6	1	Lung	O 4:451
21.2-14.2	D3S32	5	1	0.2	Lung	GCC 11:15
21.2-14.2	D3S32	4	4	1	Lung	CR 52:873
21.2-14.2	D3S32	17	10	0.59	Melanoma	GCC 15:102
21.2-14.2	D3S32	13	2	0.15	Ovary	IJC 54:546
21.2-14.2	D3S32	17	3	0.18	Ovary	CR 51:5118
21.2-14.2	D3S32	17	3	0.18	Ovary	CR 51:5118
21.2-14.2	D3S32	3	1	0.33	Pancreas	CR 54:2761
21.2-14.2	D3S32	10	1	0.1	Prostate	PNAS 87:875
21.2-14.2	D3S32	10	1	0.1	Prostate	CSurveys 11
21.2-14.2	D3S32	33	15	0.45	Testis	O 9:2245
21.2-14.2	D3S32	4	2	0.5	Uterus	GCC 9:119
21.2-21.1	D3S1289	15	5	0.33	Melanoma	GCC 15:102
21.32-21.33	D3S643	14	4	0.29	Breast	CR 51:5794
21.32-21.33	D3S643	19	0	0	Esophageal	CR 54:6484
21.32-21.33	D3S643	3	3	1	Kidney	CR 51:4707
21.32-21.33	D3S643	17	4	0.24	Leukemia	B 83:3449
21.32-21.33	D3S643	6	3	0.5	Lung	CR 52:873
21.32-21.33	D3S643	3	3	1	Lung	CR 52:873
21	D3F152	15	7	0.47	Breast	GE 5:554
21	D3F152	33	5	0.15	Breast	CR 53:4356

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21	D3F15S2	2	0	0	Cervix	CR 49:3598
21	D3F15S2	5	3	0.6	Cervix	IJC 58:787
21	D3F15S2	21	17	0.81	Esophageal	EJC 30B:248
21	D3F15S2	12	9	0.75	Head&Neck	C 72:881
21	D3F15S2	4	2	0.5	Head&Neck	CGC 54:91
21	D3F15S2	3	3	1	Kidney	CGC 32:281
21	D3F15S2	3	0	0	Kidney	G 11:537
21	D3F15S2	24	14	0.58	Kidney	
21	D3F15S2	7	1	0.14	Kidney	
21	D3F15S2	13	10	0.77	Kidney	CR 49:1390
21	D3F15S2	21	16	0.76	Kidney	PNAS 85:157
21	D3F15S2	9	9	1	Kidney	N 327:721
21	D3F15S2	2	1	0.5	Kidney	CR 51:949
21	D3F15S2	16	12	0.75	Kidney	
21	D3F15S2	12	0	0	Lung	N 329:451
21	D3F15S2	9	9	1	Lung	N 329:451
21	D3F15S2	7	3	0.43	Lung	GCC 11:15
21	D3F15S2	1	0	0	Lung	N 329:451
21	D3F15S2	7	2	0.29	Lung	CL 51:133
21	D3F15S2	8	3	0.38	Lung	PNAS 86:509
21	D3F15S2	8	2	0.25	Lung	GCC 3:358
21	D3F15S2	6	3	0.5	Lung	PNAS 86:509
21	D3F15S2	2	0	0	Lung	PNAS 86:509
21	D3F15S2	2	0	0	Lung	CL 51:133
21	D3F15S2	2	0	0	Lung	O 4:451
21	D3F15S2	5	4	0.8	Lung	GCC 1:95
21	D3F15S2	1	0	0	Lung	NEJ 317:110
21	D3F15S2	5	3	0.6	Lung	GCC 1:95
21	D3F15S2	7	4	0.57	Lung	GCC 1:95
21	D3F15S2	1	0	0	Lung	GCC 1:95
21	D3F15S2	1	0	1	Lung	CR 49:5130
21	D3F15S2	2	2	1	Lung	GCC 1:95
21	D3F15S2	16	11	0.69	Lung	GCC 15:102
21	D3F15S2	12	7	0.58	Melanoma	O 5:219
21	D3F15S2	8	1	0.12	Ovary	IJC 52:575
21	D3F15S2	22	4	0.18	Ovary	IJC 54:546
21	D3F15S2	22	4	0.18	Ovary	BJC 69:429
21	D3F15S2	12	2	0.17	Ovary	CCG 52:72
21	D3F15S2	3	0	0	Testis	CCG 52:72
21	D3F15S2	1	0	0	Testis	CCG 52:72
21	D3F15S2	2	0	0	Testis	GCC 13:249
21	D3F15S2	18	2	0.11	Testis	CR 51:5632
21	D3F15S2	2	0	0	Uterus	CR 51:5632
21	D3F15S2	2	0	0.07	Esophageal	BJC 73:366
Unknown	D3S1076	29	2	0.29	Esophageal	CR 54:6484
Unknown	D3S1076	14	1	0.59	Kidney	BJC 69:230
Unknown	D3S1076	22	13	0	Lung	CR 52:873
Unknown	D3S965	4	0	0	Lung	CR 52:873
Unknown	D3S965	1	1	1	Lung	CR 52:873

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21.2	D3S660	33	6	0.18	Breast	CR 51:5794
Unknown	D3S660	6	2	0.33	Kidney	CR 51:4707
Unknown	D3S660	12	5	0.42	Lung	CR 52:873
Unknown	D3S660	8	8	1	Lung	CR 52:873
Unknown	D3S717	6	3	0.5	Kidney	CR 51:4707
Unknown	D3S717	4	2	0.5	Lung	CR 52:873
Unknown	D3S717	4	4	1	Lung	CR 52:873
Unknown	D3S936	11	4	0.36	Kidney	CR 51:4708
Unknown	D3S936	12	5	0.42	Lung	CR 52:873
Unknown	D3S936	4	4	1	Lung	CR 52:873
14.2-21.1	D3S1313	54	11	0.2	Esophageal	IJC 69:1
14.2-21.1	D3S1300	53	19	0.36	Esophageal	IJC 69:1
14.2-14.3	D3S678	50	19	0.38	Breast	CR 51:5794
14.2-14.3	D3S678	10	7	0.7	Kidney	CR 51:4707
Unknown	D3S687	25	8	0.32	Breast	CR 51:5794
Unknown	D3S687	13	8	0.62	Kidney	CR 51:4707
Unknown	D3S687	4	4	1	Lung	CR 52:873
Unknown	D3S687	15	3	0.2	Lung	CR 52:873
Unknown	D3S1228	31	4	0.13	Esophageal	BJC 73:366
25	D3S1228	18	8	0.44	Esophageal	CR 54:6484
25	D3S1228	26	12	0.46	Kidney	BJC 69:230
25	D3S1228	6	4	0.67	Lung	JAMA 273:55
25	D3S1228	1	1	1	Lung	JAMA 273:55
14.1-14.2	D3S1285	47	18	0.38	Esophageal	IJC 69:1
14.1-14.2	D3S1285	10	7	0.7	Melanoma	GCC 15:102
Unknown	D3S714	24	1	0.04	Breast	CR 51:5794
Unknown	D3S714	9	3	0.33	Lung	CR 52:873
14-13	D3S1217	28	18	0.64	Esophageal	C 73:2472
14-13	D3S1217	28	18	0.64	Head&Neck	CA 73:2472
Unknown	D3S1079	25	4	0.16	Esophageal	BJC 73:366
Unknown	D3S1079	11	4	0.36	Esophageal	CR 54:6484
Unknown	D3S1261	20	8	0.4	Cervix	CR 56:197
Unknown	D3S13	2	0	0	Stomach	RG 89:445
12-14.2	D3S1296	57	17	0.3	Esophageal	IJC 69:1
Unknown	D3S659	54	23	0.43	Breast	CR 51:5794
Unknown	D3S659	7	6	0.86	Cervix	GCC 9:119
Unknown	D3S659	28	10	0.36	Esophageal	GCC 10:177
Unknown	D3S659	36	6	0.17	Esophageal	BJC 73:366
Unknown	D3S659	17	7	0.41	Esophageal	CR 54:6484
Unknown	D3S659	11	8	0.73	Kidney	CR 51:4707
Unknown	D3S659	40	18	0.45	Kidney	BJC 69:230
Unknown	D3S659	17	5	0.29	Lung	CR 52:873
Unknown	D3S659	10	9	0.9	Lung	CR 52:873
Unknown	D3S659	6	0	0	Ovary	CR 51:5118
Unknown	D3S659	6	0	0	Ovary	CR 51:5118
Unknown	D3S659	11	5	0.45	Uterus	GCC 9:119

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Unknown	D3S659	14	1	0.07	Uterus	CR 54:4294
13	D3S693	6	0	0	Breast	CR 51:5794
13	D3S693	1	0	0	Lung	CR 52:5735
14	D3S6	32	11	0.34	Breast	CR 54:499
14	D3S6	5	2	0.4	Kidney	CR 49:1390
14	D3S6	3	0	0	Kidney	PNAS 85:157
14	D3S6	3	1	0.33	Kidney	GCC 11:537
14	D3S6	8	7	0.88	Lung	GCC 1:95
14	D3S6	6	2	0.33	Lung	GCC 1:95
14	D3S6	4	2	0.5	Lung	GCC 11:15
21-3	TTT12H3	66	55	0.83	Lung	CR 54:497
Unknown	D3S30	37	15	0.41	Breast	CR 54:3021
13	D3S30	18	0	0	Breast	CR 48:165
Unknown	D3S30	17	6	0.35	Cervix	IJC 58:787
Unknown	D3S30	19	6	0.32	Esophageal	CR 51:2498
13	D3S30	32	12	0.38	Esophageal	BJC 73:366
Unknown	D3S30	16	0	0.5	Kidney	CR 51:820
13	D3S30	18	9	0.5	Kidney	CR 51:820
Unknown	D3S30	12	3	0.25	Lung	CR 52:273
13	D3S30	7	1	0.14	Lung	GCC 11:15
Unknown	D3S30	11	11	1	Lung	CR 52:273
13	D3S30	7	7	1	Lung	GCC 1:240
Unknown	D3S30	11	8	0.73	Melanoma	GCC 15:102
13	D3S30	14	1	0.07	Ovary	CR 51:5118
13	D3S30	14	1	0.07	Ovary	CR 51:5118
Unknown	D3S30	12	1	0.08	Ovary	BJC 69:429
13	D3S30	18	0	0	Testis	G 5:134
13-14	D3S1284	19	12	0.63	Head&Neck	CR 54:1152
13-14	D3S1284	3	0	0	Kidney	GCC 12:76
Unknown	D3S738	3	3	1	Lung	GCC 5:119
Unknown	D3S625	2	2	1	Lung	GCC 5:119
Unknown	D3S742	4	3	0.75	Lung	GCC 5:119
Unknown	D3S739	5	3	0.6	Lung	GCC 5:119
Unknown	D3S740	5	4	0.8	Lung	GCC 5:119
Unknown	D3S216	1	1	1	Lung	GCC 5:119
Unknown	D3S733	3	3	1	Lung	GCC 5:119
13	D3S4	16	7	0.44	Kidney	CR 51:949
13	D3S4	17	4	0.24	Kidney	CR 51:1071
13	D3S4	14	8	0.57	Kidney	CR 49:1390
13	D3S4	6	5	0.83	Lung	GCC 1:240
Unknown	D3S743	5	4	0.8	Lung	GCC 5:119
Unknown	D3S759	7	6	0.86	Lung	GCC 5:119
Unknown	D3S640	5	3	0.6	Lung	GCC 5:119
Unknown	D3S1090	2	2	1	Lung	GCC 5:119
Unknown	D3S1090	2	2	1	Lung	GCC 5:119
Unknown	D3S:1067-1228	29	9	0.31	Bladder	CR 55:5213

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Unknown	RAF1-DNF15S2	25	12	0.48	Bladder	CR 51:5405
24-26	Unknown	28	13	0.46	Breast	JNCI 84:506
Unknown	D3S2-H3H2	37	12	0.32	Breast	CR 54:3021
Unknown	DNF15S2	4	1	0.25	Breast	CR 53:3804
24	EABMD	67	26	0.39	Breast	CR 54:499
Unknown	RAF1-DNF15S2	15	7	0.47	Breast	GE 5:554
Unknown	D3S663	6	3	0.5	Cervix	GCC 9:119
21.1-14.2	D3S1067	20	7	0.35	Esophageal	CR 54:6484
Unknown	D3S1110	17	7	0.41	Esophageal	CR 54:6484
Unknown	D3S1111	11	1	0.09	Esophageal	CR 54:6484
Unknown	D3S192	34	8	0.24	Esophageal	BJC 73:366
Unknown	D3S656	19	8	0.42	Esophageal	CR 54:6484
Unknown	D3S663	22	2	0.09	Esophageal	CR 54:6484
Unknown	D3S966	38	9	0.24	Esophageal	BJC 73:366
Unknown	D3S966	19	5	0.26	Esophageal	CR 54:6484
21.1-14.2	D3S1067	41	20	0.49	Kidney	BJC 69:230
25-26	D3S1085	3	3	1	Kidney	CR 51:4707
Unknown	D3S1110	15	11	0.73	Kidney	BJC 69:230
Unknown	D3S1263-D3S1307-D3S1297	22	9	0.41	Kidney	PNAS 92:285
Unknown	D3S1263-D3S1307-D3S1297	6	0	0	Kidney	PNAS 92:285
Unknown	D3S22	9	7	0.78	Kidney	CR 51:1071
25	D3S649	11	7	0.64	Kidney	CR 51:4707
Unknown	D3S654	13	4	0.31	Kidney	CR 51:4707
Unknown	D3S656	7	4	0.57	Kidney	CR 51:4707
25	D3S689	1	0	0	Kidney	CR 51:4707
25-26	D3S858	11	5	0.45	Kidney	CR 51:4707
21.1-21.2	D3S898	8	7	0.88	Kidney	CR 51:4707
14.1-14.2	D3S907	6	2	0.33	Kidney	CR 51:4707
12	D3S960	2	2	1	Kidney	CR 51:4707
Unknown	D3S:1263-1307-1297	33	10	0.3	Kidney	CR 55:6189
Unknown	DNF15S2	28	25	0.89	Kidney	CR 51:1071
Unknown	DNF15S2	19	9	0.47	Kidney	CR 51:1544
Unknown	ERBA-B	18	17	0.94	Kidney	CR 51:1071
Unknown	ERBA-B	2	0	0	Kidney	CR 51:1071
Unknown	RAF1-DNF15S2	13	7	0.54	Kidney	CR 51:949
25-26	VHL	19	16	0.84	Kidney	CR 54:2852
Unknown	Unknown	27	25	0.93	Lung	CR 54:2322
21.3	D3S1339	12	11	0.92	Lung	IJC 64:371
21	D3S48	5	5	1	Lung	GCC 5:119
Unknown	D3S654	9	7	0.78	Lung	CR 52:873
Unknown	D3S654	22	8	0.36	Lung	CR 52:873
Unknown	DNF15S2	5	1	0.2	Lung	NEJ 317:110
Unknown	DNF15S2	2	1	0.5	Lung	NEJ 317:110
Unknown	DNF15S2	5	5	1	Lung	NEJ 317:110

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Unknown	IT1H1-D3S1339-1007	7	7	1	Lung	CR 55:5133
Unknown	RAF1-DNF15S2	4	4	1	Lung	GCC 5:119
Unknown	RAF1-DNF15S2	6	3	0.5	Lung	PNAS 86:509
Unknown	RAF1-DNF15S2	5	3	0.6	Lung	PNAS 86:509
Unknown	RAF1-DNF15S2	17	8	0.47	Lung	GCC 1:358
25-24	D3S1252	5	1	0.2	Melanoma	GCC 15:102
all	7 loci	46	11	0.24	Ovary	CR 53:4456
21	D3S2-D3S86	23	0	0	Ovary	CR 53:2393
Unknown	D3S1270-11	14	2	0.14	Ovary	BJC 72:1330
Unknown	Unknown	19	2	0.11	Testis	G 5:134
21-1-14-2	D3S1067	25	3	0.12	Uterus	CR 54:4294
Unknown	D3S663	10	2	0.2	Uterus	GCC 9:119
SDH		5933	2353	0.4		

Chromosome 3 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Refere
11.0-12.0	GPX1	19	17	0.89	Kidney	Cr 15
11.0-12.0	GPX1	6	6	1	Lung	Cr 15
11.0-12.0	GPX1	3	3	1	Lung	Cr 15
12	D3S1	7	0	0	Head&Neck	CGC 5
12	D3S1	2	0	0	Kidney	CGC 3
12	D3S1	4	0	0	Lung	NEJ 3
12	D3S1	4	0	0	Lung	O 44
12	D3S1	1	0	0	Lung	N 329
12	D3S1	9	2	0.22	Lung	N 329
12	D3S1	1	0	0	Lung	N 329
12	D3S1	19	2	0.11	Ovary	ITC 9
12	D3S1	8	1	0.12	Testis	GCC 1
Unknown	D3S1764	24	1	0.04	Esophageal	BJC 7
Unknown	D3S196	31	3	0.1	Esophageal	BJC 7
Unknown	D3S196	19	9	0.47	Head&Neck	CR 54
Unknown	D3S196	19	5	0.26	Ovary	BJC 6
Unknown	D3S196	22	2	0.09	Uterus	CR 54
Unknown	CP	7	1	0.14	Lung	N 329
Unknown	CP	1	0	0	Lung	N 329
Unknown	CP	1	0	0	Lung	N 329
Unknown	D3S1268	24	2	0.08	Head&Neck	CR 54
Unknown	D3S1268	34	0	0	Head&Neck	CR 54
Unknown	D3S1268	35	5	0.14	Melanoma	CR 56
Unknown	D3S1262	37	8	0.22	Cervix	CR 56
Unknown	D3S1262	18	1	0.06	Esophageal	CR 54
28	SST	6	0	0	Cervix	CR 49
28	SST	6	0	0	Liver	CCG
28	SST	9	2	0.22	Lung	N 329
28	SST	12	0	0	Lung	PNAS
28	SST	1	0	0	Lung	N 329
28	SST	7	0	0	Lung	CR 49
28	SST	1	0	0	Melanoma	N 329
28	SST	3	0	0	Neuroblastom	CR 49
Unknown	D3S1314	26	1	0.04	Kidney	PNAS
Unknown	D3S42	4	1	0.25	Breast	CR 53
Unknown	D3S42	26	3	0.12	Breast	GCC 4
Unknown	D3S42	28	9	0.32	Cervix	CR 54
Unknown	D3S42	12	0	0	Stomach	HG 92
Unknown	D3S42	34	9	0.26	Testis	O 92
Unknown	D3S42	16	0	0	Testis	LI 73
Unknown	D3S44	35	6	0.17	Ovary	CR 53
Unknown	D3S46	19	5	0.26	Esophageal	CR 54
Unknown	D3S46	0	3	0	Esophageal	Unkno
Unknown	D3S46	44	13	0.3	Esophageal	GCC 1
Unknown	D3S46	16	3	0.19	Kidney	CR 54

Chromosome 3 - q Arm

Unknown	D3S46	7	0	0	Liver	CR 51
Unknown	D3S46	40	6	0.15	Lung	CR 52
Unknown	D3S46	18	1	0.06	Ovary	CR 51
Unknown	D3S46	18	1	0.06	Ovary	CR 51
Unknown	D3S46	3	0	0	Pancreas	CR 54
Unknown	D3S46	12	8	0.75	Sarcoma	CR 52
Unknown	D3S46	12	9	0.75	Sarcoma	CR 52
Unknown	Unknown	13	0	0	Brain	CR 50
21-qter	D3S5	1	0	0	Brain	CCG 5
Unknown	MOX2	1	0	0	Brain	CCG 5
Unknown	D3S47	21	0	0	Endocrine	GCC 1
Unknown	GLUT2	23	0	0	Endocrine	GCC 1
Unknown	D3S1271	14	1	0.07	Esophageal	CR 54
Unknown	D3S1238	20	7	0.35	Head/Neck	CR 54
Unknown	D3S1-MOX2-D3S5	24	2	0.08	Kidney	G 11:
Unknown	D3S31	14	0	0	Kidney	CR 49
26.2-qTER	D3S45	20	3	0.15	Kidney	CR 51
all	4 markers	32	15	0.41	Lung	GCC 1
12-q13	MOX1	15	7	0.47	Lung	GCC 1
12-q13	MOX1	6	2	0.33	Lung	GCC 1
12-q13	MOX1	1	1	1	Lung	GCC 1
12-q13	MOX1	1	1	1	Lung	GCC 1
all	4 markers	46	8	0.17	Ovary	CR 53
21-PTER	ACCE	13	4	0.31	Ovary	BJC 6
Unknown	D3S1232-GLUT2	14	2	0.14	Ovary	BJC 7
Unknown	D3S31	13	0	0	Prostate	G 11:
SUM		1050	191	0.18		

Chromosome 4 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
16.1	RAF1P1	7	0	0	Uterus	CR 51:5632
Unknown	D4S1546	25	8	0.32	Bladder	CR 55:5213
Unknown	D4S124	16	0	0	Brain	CR 50:5784
16	D4S10	31	0	0	Breast	GE 5:554
pter-16.3	D4S125	6	1	0.17	Breast	CR 50:7184
16	D4S95	33	4	0.12	Breast	CR 53:4356
pter-16.3	D4S125	9	0	0	Cervix	CR 54:4481
Unknown	D4S125	2	0	0	Cervix	GCC 9:119
Unknown	D4S391	25	9	0.36	Cervix	CR 56:197
Unknown	D4S405	30	4	0.13	Cervix	CR 56:197
16	D4S10	11	0	0	Colon	CCG 48:167
pter-16.3	D4S125	8	0	0	Colon	CCG 48:167
11.0-15	D4S174	21	0	0	Endocrine	GCC 13:9
Unknown	D4S2397	18	1	0.06	Endocrine	CR 56:599
Unknown	D4S124	21	2	0.1	Esophageal	CR 54:2996
Unknown	D4S125	40	7	0.17	Esophageal	GCC 10:177
pter-16.3	D4S125	9	0	0	Esophageal	CR 51:2113
Unknown	D4S394	15	1	0.07	Head&Neck	CR 54:4756
Unknown	D4S394	18	0	0	Head&Neck	CR 54:4756
Unknown	D4S404	21	8	0.38	Head&Neck	CR 54:1152
pter-16.3	D4S125	7	0	0	Kidney	CR 51:820
Unknown	D4S431	28	2	0.07	Kidney	PNAS 92:2854
16.3	D4S10	5	1	0.2	Liver	CCG 48:72
16	D4S10	6	2	0.33	Liver	CR 51:4367
pter-16.3	D4S125	4	0	0	Liver	CR 51:89
Unknown	D4S125	6	0	0	Liver	PNAS 86:8852
16.1	RAF1P1	13	2	0.15	Liver	IJCR 81:108
pter-16.3	D4S125	28	2	0.07	Lung	CR 52:2478
pter-16.3	D4S125	24	10	0.42	Ovary	CR 51:5118
Unknown	D4S125-D4S124	29	10	0.34	Ovary	CR 53:2393
15.1-11	D4S16	19	2	0.11	Ovary	IJC 54:546
11.0-15	D4S174	20	3	0.15	Ovary	BJC 69:429
16.2-15.1	D4S49	20	5	0.25	Ovary	IJC 54:546
12.0-13	GABRB1	16	2	0.12	Ovary	BJC 69:429
pter-16.3	D4S125	3	0	0	Pancreas	CR 54:2761
12.0-13	GABRB1	13	0	0	Prostate	G 11:530
Unknown	D4S124	13	1	0.08	Sarcoma	CR 52:2419
Unknown	D4S125	17	3	0.18	Testis	O 9:2245
pter-16.3	D4S125	9	0	0	Testis	LI 73:606
Unknown	D4S129	10	1	0.1	Testis	GCC 13:249
pter-16.3	D4S125	2	0	0	Uterus	GCC 9:119
11.0-15	D4S174	21	1	0.05	Uterus	CR 54:4294
16	D4S43	25	1	0.04	Uterus	CR 54:4294
12.0-13	GABRB1	25	0	0	Uterus	CR 54:4294
16.1	RAF1P1	7	0	0	Uterus	CR 51:5632

Chromosome 4 - p Arm

SUM	729	93	0.13
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Chromosome 4 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
p11-q21	MT2P1	4	0	0	Uterus	CR 51:5632
33-35	D4S171	29	15	0.52	Bladder	CR 55:5213
25-34	D4S243	29	15	0.52	Bladder	CR 55:5213
Unknown	Unknown	20	2	0.1	Brain	CR 50:5784
Unknown	D4S125	34	2	0.06	Breast	CR 50:7184
25-34	D4S192	54	13	0.24	Breast	BCRT 32:5
28	FGA	19	4	0.21	Breast	GCC 2:191
28	FGA	18	0	0	Breast	CR 53:4356
p11-q21	MT2P1	17	0	0	Breast	JNCI 84:506
21-23	ADH3	22	12	0.55	Cervix	CR 54:4481
21-23	ADH5	24	11	0.46	Cervix	CR 54:4481
Unknown	D4S163	41	12	0.29	Cervix	CR 54:4481
Unknown	D4S402	28	8	0.29	Cervix	CR 56:197
Unknown	D4S415	26	8	0.31	Cervix	CR 56:197
q11-q13	ALB	11	0	0	Colon	CCG 48:167
Unknown	D4S415	19	1	0.05	Endocrine	CR 56:599
Unknown	D4S163	21	2	0.1	Esophageal	CR 51:2996
Unknown	D4S163	35	9	0.26	Esophageal	GCC 10:177
Unknown	D4S402	16	3	0.19	Head&Neck	CR 54:4756
Unknown	D4S402	20	1	0.05	Head&Neck	CR 54:4756
Unknown	D4S430	24	9	0.38	Head&Neck	CR 54:1152
Unknown	D4S163	23	2	0.09	Kidney	CR 51:820
Unknown	D4S426-D4S415	20	1	0.05	Kidney	PNAS 92:2854
Unknown	D4S426-D4S415	5	0	0	Kidney	PNAS 92:2854
Unknown	D4S1408-429	23	4	0.17	Leukemia	CR 55:5377
Unknown	Unknown	8	0	0	Liver	BJC 64:1083
21-23	ADH3	4	0	0	Liver	JJCR 81:108
21-23	ADH3	6	1	0.17	Liver	CR 51:4367
q11-q13	ALB	5	5	1	Liver	PNAS 86:8852
Unknown	D4S16	5	2	0.4	Liver	JJCR 81:108
Unknown	D4S163	20	3	0.15	Liver	CR 51:89
p11-q21	MT2P1	16	8	0.5	Liver	JJCR 81:108
p11-q21	MT2P1	21	9	0.43	Liver	JJCR 84:893
p11-q21	MT2P1	19	4	0.21	Liver	CR 54:281
Unknown	D4S163	31	6	0.26	Lung	CR 52:2478
21-23	ADH3	18	1	0.06	Ovary	IJC 54:546
11.0-15	D4S1540	20	3	0.15	Ovary	BJC 69:429
11.0-15	D4S1607	20	3	0.15	Ovary	BJC 69:429
Unknown	D4S163	16	1	0.06	Ovary	CR 51:5318
33-35	D4S171	12	4	0.33	Ovary	BJC 69:429
25-34	D4S175	20	7	0.35	Ovary	BJC 69:429
Unknown	D4S27	29	10	0.34	Ovary	CR 53:2393
p11-q21	MT2P1	21	2	0.1	Ovary	IJC 54:546
35	Unknown	6	1	0.17	Pancreas	CR 54:2761
28	FGA	9	0	0	Prostate	G 17:530
Unknown	D4S163	17	3	0.18	Sarcoma	CR 52:2419

Chromosome 4 - q Arm

21-23	ADH3	24	0	0	Testis	0.9:2245
33-35	D4S171	23	0	0	Uterus	CR 54:4294
p11-q21	MT2P1	4	0	0	Uterus	CR 51:5632
SUM		952	209	0.22		

Chromosome 5 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D5S392	34	8	0.24	Cervix	JNCI 87:742
Unknown	D5S392	19	0	0	Endocrine	CR 56:599
Unknown	D5S392	26	5	0.19	Head&Neck	CR 54:1152
Unknown	D5S392	19	0	0	Kidney	PNAS 92:2854
Unknown	D5S392	5	0	0	Kidney	PNAS 92:2854
Unknown	D5S13	21	1	0.05	Breast	CR 53:4356
Unknown	D5S13	17	4	0.24	Breast	GCC 2:191
pter-p15	D5S4	10	1	0.1	Breast	GCC 2:191
pter-p15	D5S4	17	2	0.12	Colon	IJC 53:382
pter-p15	D5S4	11	0	0	Colon	CCG 48:167
pter-p15	D5S4	29	1	0.03	Colon	CR 50:7166
pter-p15	D5S4	19	4	0.21	Ovary	CR 53:2393
pter-p15	D5S4	3	0	0	Testis	CCG 52:72
pter-p15	D5S4	1	0	0	Testis	CCG 52:72
pter-p15	D5S4	1	0	0	Testis	CCG 52:72
15.1-15.2	D5S406	25	12	0.48	Cervix	JNCI 87:742
15.2-15.1	D5S12	12	1	0.08	Brain	CR 50:5784
15.2-15.1	D5S12	13	5	0.38	Cervix	CR 54:4481
15.2-15.1	D5S12	9	0	0	Ovary	O 5:219
15.2-15.1	D5S12	17	0	0	Prostate	G 11:530
15.2-15.1	D5S12	26	11	0.42	Testis	O 9:2245
15.1-15.3	D5S208	20	10	0.5	Cervix	JNCI 87:742
15-21	D5S630	5	2	0.4	Lung	O 12:97
15-21	D5S630	13	3	0.23	Lung	O 12:97
14	D5S432	29	8	0.28	Cervix	JNCI 87:742
15.1-15.3	D5S117	25	8	0.32	Cervix	JNCI 87:742
15.1-15.3	D5S117	13	2	0.15	Ovary	BJC 69:429
15.1-15.3	D5S117	22	1	0.05	Uterus	CR 54:4294
Unknown	D5S268	14	3	0.21	Ovary	BJC 69:429
Unknown	D5S419	26	3	0.12	Cervix	CR 56:197
Unknown	D5S419	28	0	0	Head&Neck	CR 54:4756
Unknown	D5S419	16	3	0.19	Head&Neck	CR 54:4756
14	D5S19	23	13	0.57	Cervix	CR 54:4481
Unknown	D5S395	28	6	0.21	Cervix	CR 56:197
13	D5S20	21	1	0.05	Ovary	IJC 54:546
11.0-13	D5S21	9	5	0.56	Cervix	CR 54:4481
11.0-13	D5S21	9	5	0.56	Cervix	CR 54:4481
Unknown	Unknown	4	0	0	Brain	CR 49:6572
Unknown	D5S1	5	1	0.2	Breast	GCC 2:191
Unknown	Unknown	5	0	0	Colon	BJC 67:1007
Unknown	D5S1	3	0	0	Colon	CCG 48:167
Unknown	D5S1	28	7	0.25	Esophageal	CR 54:2996
Unknown	Unknown	4	0	0	Liver	BJC 67:1007
Unknown	Unknown	8	3	0.38	Liver	BJC 64:1083
Unknown	Unknown	3	0	0	Pancreas	CR 54:2761
Unknown	Unknown	7	0	0	Pancreas	BJC 65:809

Chromosome 5 - p Arm

Unknown	Unknown	29	1	0.03	Testis	GCC 13:249
SUM		722	135	0.19		

Chromosome 5 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
15-21	D5S491	1	0	0	Lung	O 12:97
15-21	D5S491	8	3	0.38	Lung	O 12:97
Unknown	D5S427	22	4	0.18	Cervix	CR 56:197
11.2-13.3	D5S6	30	1	0.03	Breast	GE 5:554
11.2-13.3	D5S6	4	2	0.5	Colon	O 9:991
11.2-13.3	D5S6	32	9	0.28	Colon	CR 50:7166
11.2-13.3	D5S6	17	1	0.06	Pediatric	CR 50:3279
15-21	D5S637	5	1	0.2	Lung	O 12:97
15-21	D5S637	9	6	0.67	Lung	O 12:97
15-21	D5S626	4	1	0.25	Lung	O 12:97
15-21	D5S626	17	9	0.53	Lung	O 12:97
Unknown	D5S107	19	2	0.11	Leukemia	B 83:3449
Unknown	D5S107	33	2	0.06	Stomach	CR 56:612
Unknown	D5S107	30	1	0.03	Uterus	CR 54:4294
Unknown	D5S428	20	7	0.35	Stomach	CR 56:612
Unknown	D5S37	2	0	0	Colon	O 9:991
Unknown	D5S37	11	6	0.55	Colon	CR 50:7166
Unknown	D5S37	28	7	0.25	Esophageal	CR 54:2996
Unknown	D5S37	3	0	0	Liver	CCG 48:72
Unknown	D5S37	12	5	0.42	Sarcoma	CR 52:2419
Unknown	D5S37	18	4	0.22	Testis	GCC 13:249
15-21	D5S644	9	3	0.33	Lung	O 12:97
15-21	D5S644	22	12	0.55	Lung	O 12:97
14-21	D5S71	10	1	0.1	Colon	S 241:961
14-21	D5S71	6	3	0.5	Colon	CR 50:7166
14-21	D5S71	8	3	0.38	Colon	GCC 3:468
14-21	D5S71	4	0	0	Colon	CCG 48:167
14-21	D5S71	21	1	0.05	Ovary	IJC 54:546
14-21	D5S71	1	1	1	Pancreas	GCC 3:468
14-21	D5S71	6	0	0	Stomach	GCC 3:468
14-21	D5S71	6	2	0.33	Testis	GCC 13:249
14-21	D5S71	1	0	0	Uterus	CR 51:5632
Unknown	D5S409	17	1	0.06	Endocrine	CR 56:599
Unknown	D5S409	17	6	0.35	Stomach	CR 56:612
Unknown	D5S409	9	6	0.67	Stomach	CR 55:1933
14-21	D5S82	15	4	0.27	Colon	JJCR 82:10
Unknown	D5S82	16	1	0.06	Stomach	CR 54:41
21	D5S421	25	5	0.2	Bladder	CR 55:5213
21	D5S421	20	5	0.25	Head&Neck	CR 54:1152
21	D5S421	5	0	0	Kidney	GCC 12:76
21-22	D5S81	13	0	0.23	Cervix	BJC 67:71
Unknown	D5S81	31	19	0.61	Colon	CR 50:7166
21-22	D5S81	5	4	0.8	Colon	BJC 67:100
21-22	D5S81	13	4	0.22	Colon	JJCR 82:10
Unknown	D5S81	28	5	0.18	Kidney	CR 51:5817
21-22	D5S81	13	3	0.23	Kidney	CR 51:820

Chromosome 5 - q Arm

21-22	D5S81	6	1	0.17	Liver	BJC 64:108
21-22	D5S81	4	0	0	Liver	BJC 67:100
21-22	D5S81	5	1	0.2	Pancreas	BJC 65:809
21-22	D5S81	12	5	0.42	Stomach	HG 92:244
Unknown	D5S81	9	2	0.22	Testis	GCC 13:249
Unknown	L5.71	13	5	0.38	Colon	JJCR 82:10
Unknown	MCC	13	5	0.38	Colon	JJCR 82:10
21	MCC	4	1	0.25	Colon	O 9:991
21	MCC	31	9	0.29	Colon	CR 52:741
21	MCC	34	12	0.35	Colon	EJC 30A:66
21	MCC	35	22	0.63	Esophageal	CR 52:6525
Unknown	L5.71	2	2	1	Lung	CR 52:2478
Unknown	L5.71	16	4	0.25	Lung	CR 52:2478
Unknown	L5.71	1	1	1	Lung	CR 52:2478
Unknown	L5.71	4	0	0	Lung	CR 52:2478
Unknown	MCC	2	2	1	Lung	CR 52:2478
21	MCC	41	9	0.22	Lung	CR 55:220
Unknown	MCC	1	1	1	Lung	CR 52:2478
Unknown	MCC	16	4	0.25	Lung	CR 52:2478
Unknown	MCC	4	0	0	Lung	CR 52:2478
21	MCC	7	7	1	Stomach	JJCR 84:10
21	MCC	36	4	0.11	Stomach	CL 96:169
21	MCC	8	0	0	Stomach	CR 54:41
21	MCC-APC	25	7	0.28	Breast	BJC 68:64
21	MCC-APC	6	0	0	Cervix	GCC 9:119
21	MCC-APC	45	16	0.36	Colon	GAST 104:1
21	MCC-APC	56	37	0.66	Colon	O 8:1391
21	MCC-APC	26	20	0.77	Esophageal	PNAS 89:33
21	MCC-APC	6	4	0.67	Lung	CR 55:513
21	MCC-APC	5	2	0.4	Lung	CR 52:1996
21	MCC-APC	7	0	0	Uterus	GCC 9:119
21	APC	21	7	0.33	Colon	CR 52:741
Unknown	APC	37	3	0.08	Colon	EJC 30A:66
Unknown	APC	33	6	0.18	Colon	EJC 30A:66
21	APC	21	5	0.24	Esophageal	GCC 10:177
21	APC	36	24	0.67	Esophageal	CR 52:6525
21	APC	19	1	0.05	Liver	CR 54:281
21	APC	20	14	0.7	Lung	O 12:97
21	APC	53	17	0.32	Lung	CR 55:220
21	APC	7	5	0.71	Lung	CR 54:1772
21	APC	8	3	0.38	Lung	O 12:97
Unknown	APC	18	9	0.5	Ovary	GO 55:245
Unknown	APC	15	3	0.2	Prostate	JU 151:107
21	APC	7	3	0.43	Prostate	BJU 73:390
Unknown	APC	13	4	0.31	Stomach	LI 74:835
Unknown	APC	35	3	0.09	Stomach	CL 96:169

Chromosome 5 - q Arm

21	APC	12	0	0	Stomach	CR 54:41
21	APC	14	12	0.86	Stomach	JJCR 84:10
21-22	D5S346	18	0	0	Endocrine	GCC 13:9
21-22	D5S346	46	1	0.02	Kidney	BJC 69:230
21-22	D5S346	15	6	0.4	Ovary	BJC 69:429
21-22	D5S346	18	2	0.11	Stomach	CR 56:612
21-22	D5S346	22	1	0.05	Uterus	CR 54:4294
Unknown	Unknown	19	3	0.16	Colon	JJCR 82:10
Unknown	Unknown	10	2	0.2	Kidney	CR 51:5817
21-22	D5S84	11	2	0.18	Breast	CR 50:7184
21-22	D5S84	21	1	0.05	Breast	CR 53:4356
21-22	D5S84	3	1	0.33	Cervix	GCC 9:119
21-22	D5S84	8	0	0	Cervix	BJC 67:71
21-22	D5S84	5	2	0.4	Kidney	CR 51:5817
21-22	D5S84	5	2	0.4	Kidney	CR 51:820
21-22	D5S84	9	4	0.44	Liver	CR 51:89
21-22	D5S84	15	0	0	Ovary	CR 51:5118
21-22	D5S84	13	1	0.08	Uterus	GCC 9:119
21-22	D5S86	6	2	0.33	Colon	GCC 3:468
21-22	D5S86	4	1	0.25	Pancreas	GCC 3:468
21-22	D5S86	8	3	0.38	Stomach	GCC 3:468
31-33	D5S804	19	6	0.32	Ovary	GO 55:245
21-22	FBN2	15	6	0.4	Ovary	BJC 69:429
21-22	FBN2	15	4	0.27	Stomach	CR 56:612
33-35	D5S70	24	9	0.38	Cervix	CR 54:4481
33-35	D5S70	3	0	0	Colon	GCC 3:468
33-35	D5S70	3	0	0	Pancreas	GCC 3:468
33-35	D5S70	13	5	0.38	Stomach	GCC 3:468
33-35	D5S70	13	3	0.23	Testis	O 9:2245
21-22	D5S178	15	6	0.4	Ovary	BJC 69:429
21-22	D5S178	19	2	0.11	Stomach	CR 56:612
31-32	GRL	8	0	0	Ovary	CR 50:2724
21-22	D5S210	15	6	0.4	Ovary	BJC 69:429
21-22	D5S210	19	5	0.26	Stomach	CR 56:612
21-22	D5S209	15	6	0.4	Ovary	BJC 69:429
21-22	D5S209	23	2	0.09	Stomach	CR 56:612
34-qter	D5S22	18	0	0	Prostate	G 11:530
34-qter	D5S2	3	1	0.33	Cervix	CR 49:3598
34-qter	D5S2	2	0	0	Colon	N 331:273
34-qter	D5S2	8	0	0	Liver	JJCR 81:10
34-qter	D5S2	11	1	0.09	Lung	PN 84:9252
Unknown	D5S2	11	1	0.09	Lung	PNAS 84:92
Unknown	D5S2	5	1	0.2	Stomach	CR 52:3099
34-qter	D5S2	2	0	0	Stomach	CR 48:2988
34-qter	D5S2	1	0	0	Uterus	CR 51:5632
Unknown	D5S400	32	5	0.16	Cervix	CR 56:197

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Unknown	D5S429	3	0	0	Kidney	PNAS 92:28
Unknown	D5S429	19	1	0.05	Kidney	PNAS 92:28
35-qter	D5S43	17	1	0.06	Colon	CR 50:7166
35-qter	D5S43	5	2	0.4	Colon	BJC 67:100
35-qter	D5S43	31	9	0.29	Colon	BJC 59:750
35-qter	D5S43	10	0	0	Endocrine	N 328:524
35-qter	D5S43	10	3	0.3	Liver	BJC 67:100
35-qter	D5S43	10	5	0.5	Liver	BJC 64:108
35-qter	D5S43	7	0	0	Pancreas	CR 54:2761
35-qter	D5S43	11	0	0	Pancreas	BJC 65:809
35-qter	D5S43	10	1	0.1	Stomach	BJC 59:750
35-qter	D5S43	34	8	0.24	Stomach	CR 51:2926
35-qter	D5S43	25	5	0.2	Testis	GCC 13:249
35-qter	D5S43	25	5	0.2	Testis	GCC 13:249
Unknown	Unknown	12	2	0.17	Brain	CR 50:5784
15-21	Unknown	6	0	0	Cervix	BJC 67:71
21	Unknown	2	0	0	Cervix	BJC 67:71
Unknown	Unknown	2	1	0.5	Cervix	BJC 67:71
Unknown	Unknown	11	2	0.18	Cervix	BJC 67:71
Unknown	Unknown	23	8	0.35	Colon	JJCR 82:10
Unknown	Unknown	2	1	0.5	Colon	JJCR 82:10
Unknown	Unknown	19	7	0.37	Colon	JJCR 82:10
Unknown	Unknown	1	1	1	Colon	JJCR 82:10
Unknown	Unknown	17	1	0.06	Colon	JJCR 82:10
Unknown	Unknown	10	5	0.5	Colon	JJCR 82:10
Unknown	Unknown	17	6	0.35	Colon	JJCR 82:10
Unknown	Unknown	3	0	0	Colon	JJCR 82:10
15-21	Unknown	1	1	1	Colon	BJC 67:100
21	Unknown	4	3	0.75	Colon	BJC 67:100
21	C11p11	3	1	0.33	Colon	N 331:273
Unknown	CRI-L1265	16	1	0.06	Colon	S 241:961
Unknown	CRI-L45	21	2	0.1	Colon	S 241:961
33	CSF1R	11	4	0.36	Colon	CR 50:7166
21	D5S141	3	2	0.67	Colon	BJC 67:100
Unknown	FMS	9	2	0.22	Colon	N 331:273
21-22	LS5.34	5	3	0.6	Colon	CR 50:7166
21	D5S141	35	13	0.37	Esophageal	GCC 10:177
Unknown	D5S410	31	1	0.03	Head&Neck	CR 54:4756
Unknown	D5S410	35	4	0.11	Head&Neck	CR 54:4756
21	D5S133	6	1	0.17	Kidney	CR 51:5817
21	D5S140	16	3	0.19	Kidney	CR 51:5817
21	D5S141	26	8	0.31	Kidney	CR 51:5817
Unknown	D5S89	15	5	0.33	Leukemia	B 83:199
Unknown	Unknown	10	1	0.1	Liver	CR 51:89
21	Unknown	6	0	0	Liver	BJC 67:100
15-21	Unknown	5	0	0	Liver	BJC 67:100

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21	D5S141	7	0	0	Liver	BJC 67:100
21-21-34-qter	D5S43-D5S81	45	14	0.31	Liver	JJCR 84:89
21	ECB27	8	1	0.12	Liver	BJC 64:108
Unknown	FMS	2	0	0	Lung	PN 84:9252
13-12	del-27	15	11	0.73	Lung	O 12:97
13-12	del-27	8	3	0.38	Lung	O 12:97
13-12	del-27	7	4	0.57	Lung	CR 54:1772
21	D5S122	11	5	0.45	Ovary	GO 55:245
Unknown	D5S6-D5S107-APC	37	16	0.43	Ovary	CR 53:2193
21-22	IRF-1	15	6	0.4	Ovary	BJC 69:429
15-21	Unknown	5	0	0	Pancreas	BJC 65:809
15-21	D5S98	13	3	0.23	Stomach	HG 92:244
21-22	IRF-1	22	6	0.27	Stomach	CR 56:612
15-21	D5S98	7	1	0.14	Testis	GCC 13:249
Unknown	FMS	21	1	0.05	Uterus	CR 54:4294
SUM		2866	763	0.27		

Chromosome 6 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D6S477	33	15	0.45	Colon	CR 56:145
24-25	F13A1	18	5	0.28	Ovary	GO 55:245
24-25	F13A1	18	4	0.22	Ovary	BJC 69:429
Unknown	D6S309	18	1	0.06	Kidney	PNAS 92:2854
Unknown	D6S309	4	1	0.25	Kidney	PNAS 92:2854
pter-p25	D6F21S1	12	4	0.33	Ovary	BJC 67:551
Unknown	D6S89	14	1	0.07	Ovary	BJC 67:551
Unknown	D6S289	36	13	0.36	Colon	CR 56:145
Unknown	D6S260	32	14	0.44	Cervix	CR 56:197
21.3-24	D6S109	17	3	0.18	Ovary	BJC 69:429
21.3-24	D6S109	16	2	0.12	Uterus	CR 54:4294
Unknown	D6S276	20	10	0.5	Cervix	CR 56:197
Unknown	D6S299	21	1	0.05	Head&Neck	CR 54:4756
Unknown	D6S299	20	0	0	Head&Neck	CR 54:4756
Unknown	D6S299	26	2	0.08	Melanoma	CR 56:589
Unknown	D6S105	27	2	0.07	Esophageal	IJC 69:1
Unknown	D6S105	19	4	0.21	Head&Neck	CR 54:1152
Unknown	D6S105	26	2	0.08	Uterus	CR 54:4294
Unknown	D6S258	33	15	0.45	Colon	CR 56:145
Unknown	D6S10	35	4	0.11	Breast	GCC 2:191
Unknown	D6S10	32	9	0.28	Cervix	CR 54:4481
Unknown	D6S10	2	0	0	Pancreas	CR 54:2761
Unknown	D6S10	13	0	0	Prostate	G 11:530
Unknown	D6S10	32	4	0.12	Testis	O 9:2245
21.3	HLA-DRB	21	3	0.14	Ovary	BJC 67:551
21.3	HLA-DQA	18	4	0.22	Ovary	BJC 67:551
21.3	HLA-DQA	3	0	0	Testis	CCG 52:72
21.3	HLA-DQA	1	0	0	Testis	CCG 52:72
21.3	HLA-DQA	4	0	0	Testis	CCG 52:72
Unknown	TNFA	33	14	0.42	Colon	CR 56:145
Unknown	D6S291	12	1	0.09	Brain	CR 55:4696
Unknown	D6S291	12	1	0.08	Brain	CR 55:4696
Unknown	D6S29	17	0	0	Colon	CCG 48:167
Unknown	D6S29	22	3	0.14	Kidney	CR 51:5817
Unknown	D6S29	13	1	0.08	Liver	CR 51:89
Unknown	D6S29	12	6	0.5	Ovary	CR 51:5118
Unknown	D6S29	19	4	0.21	Ovary	IJC 54:546
Unknown	D6S29	9	0	0	Ovary	CR 50:2724
Unknown	D6S29	16	3	0.19	Stomach	GCC 14:28
Unknown	D6S271	44	17	0.39	Colon	CR 56:145
Unknown	D6S282	32	6	0.19	Cervix	CR 56:197
Unknown	D6S282	22	0	0	Endocrine	CR 56:599
12.0-11	KRAS P1	8	1	0.12	Ovary	BJC 67:551
12.0-11	KRAS P1	2	0	0	Uterus	CR 51:5632
11.2	D6S294	37	11	0.3	Ovary	GCC 15:223
Unknown	D6S257	42	13	0.31	Colon	CR 56:145

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Unknown	D6S257	42	13	0.31	Colon	CR 56:145
Unknown	Unknown	14	1	0.07	Brain	CR 50:5783
Unknown	D6S40	24	2	0.08	Brain	CR 49:6572
Unknown	D6S40	28	5	0.18	Breast	CR 50:7184
Unknown	D6S40	3	1	0.33	Cervix	GCC 9:119
Unknown	D6S344	22	0	0	Endocrine	CR 56:599
Unknown	D6S139	49	12	0.24	Esophageal	GCC 10:177
Unknown	D6S40	23	7	0.3	Esophageal	CR 54:2996
Unknown	D6S40	14	1	0.07	Esophageal	CR 51:2113
Unknown	D6S265	19	8	0.42	Head&Neck	CR 54:1152
Unknown	TCTE	14	2	0.14	Head&Neck	CR 54:1152
21.3	D6S138	34	6	0.18	Kidney	CR 51:5817
21.2	D6S160	23	5	0.22	Kidney	CR 51:5817
Unknown	D6S4-C2-D6S1	19	5	0.26	Kidney	CR 49:5087
Unknown	D6S40	14	3	0.21	Kidney	CR 51:820
Unknown	Unknown	20	15	0.75	Lung	CR 54:2322
Unknown	D6S4-C2-D6S1	1	1	1	Lung	CR 49:5087
Unknown	D6S40	22	4	0.18	Lung	CR 52:2478
21-27	Unknown	7	2	0.29	Ovary	O 5:219
Unknown	D6S114E	3	0	0	Ovary	BJC 67:551
Unknown	D6S40	7	4	0.57	Ovary	O 5:219
Unknown	F13A1-D6S249	17	4	0.24	Ovary	BJC 72:1330
12-21.3	FTHP1	14	5	0.36	Ovary	BJC 69:429
12-21.2	FTHP1	10	2	0.2	Ovary	BJC 67:551
Unknown	P1M-HLA-D6S91-D6S41	34	21	0.62	Ovary	CR 53:2393
Unknown	D6S4-C2-D6S1	2	1	0.5	Sarcoma	CR 49:5087
Unknown	D6S40	13	7	0.54	Sarcoma	CR 52:2419
21.3	HLA-DXA	2	0	0	Testis	CCG 52:72
21.3	HLA-DXA	2	0	0	Testis	CCG 52:72
21.3	HLA-DXA	1	0	0	Testis	CCG 52:72
Unknown	D6S40	5	0	0	Uterus	GCC 9:119
SUM		1383	328	0.24		

Chromosome 6 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D6Z1	8	2	0.25	Ovary	BJC 67:551
Unknown	D6Z1	22	0	0	Stomach	GCC 14:28
13	D6S313	30	3	0.1	Breast	BJC 71:290
13	D6S254	5	0	0	Breast	BJC 73:144
13	D6S280	20	8	0.4	Breast	BJC 71:290
14-15	D6S284	26	5	0.19	Breast	BJC 71:290
14-15	D6S284	5	1	0.2	Breast	BJC 73:144
16.3-21	D6S286	27	8	0.3	Breast	BJC 71:290
14-15	D6S286	11	4	0.36	Breast	BJC 73:144
16.3-21	D6S286	17	1	0.06	Endocrine	CR 56:599
14-15	D6S286	17	8	0.47	Ovary	GCC 15:223
Unknown	EDDR1	14	4	0.29	Ovary	GCC 15:223
22.3-23.1	D6S270	5	1	0.2	Breast	BJC 73:144
22.3-23.1	D6S270	22	7	0.32	Ovary	GCC 15:223
Unknown	D6S310	23	7	0.3	Endocrine	CR 56:599
Unknown	D6S310	33	10	0.3	Ovary	GCC 15:223
Unknown	D6S311	27	5	0.19	Cervix	CR 56:197
Unknown	D6S311	6	4	0.67	Endocrine	CR 56:599
Unknown	D6S311	32	10	0.31	Ovary	GCC 15:223
Unknown	D6S194	4	0	0	Ovary	CR 52:5815
Unknown	D6S194	16	5	0.31	Ovary	GCC 15:223
Unknown	D6S194	16	4	0.25	Ovary	CR 52:5815
Unknown	D6S142	30	8	0.27	Kidney	CR 51:5817
Unknown	D6S142	6	0	0	Ovary	CR 52:5815
Unknown	D6S142	12	7	0.58	Ovary	CR 52:5815
Unknown	D6S142	6	0	0	Ovary	CR 52:5815
Unknown	D6S161	27	6	0.22	Kidney	CR 51:5817
Unknown	D6S161	11	0	0	Ovary	CR 52:5815
Unknown	D6S161	17	7	0.41	Ovary	CR 52:5815
Unknown	D6S161	5	1	0.2	Ovary	CR 52:5815
Unknown	D6S251	67	16	0.24	Breast	BJC 73:144
Unknown	D6S251	36	13	0.36	Colon	CR 56:145
Unknown	D6S251	5	0	0	Ovary	CR 55:2169
Unknown	D6S251	28	0	0	Ovary	CR 55:2169
13	D6S239	27	9	0.33	Breast	BJC 71:290
13	D6S239	10	3	0.3	Ovary	CR 55:2169
13	D6S239	27	1	0.04	Ovary	CR 55:2169
14-16.2	D6S252	48	11	0.23	Breast	BJC 73:144
14-16.2	D6S252	27	2	0.07	Stomach	GCC 14:28
14	D6S300	32	11	0.34	Breast	BJC 71:290
14	D6S300	17	3	0.18	Endocrine	CR 56:599
16.3	D6S246	27	9	0.33	Breast	BJC 71:290
Unknown	D6S246	16	1	0.06	Ovary	CR 55:2169
Unknown	D6S246	9	2	0.22	Ovary	CR 55:2169
16.3-21	D6S249	28	9	0.32	Breast	BJC 73:144
16.3-21	D6S283	30	5	0.17	Breast	BJC 71:290

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16.3-21	D6S283	10	2	0.2	Stomach	GCC 14:28
Unknown	D6S268	4	1	0.25	Kidney	GCC 12:76
Unknown	D6S268	9	1	0.11	Stomach	GCC 14:28
16.3-21	D6S302	30	13	0.43	Breast	BJC 73:144
21-23.3	D6S261	34	7	0.21	Breast	BJC 71:290
21-23	D6S261	25	5	0.2	Breast	BJC 73:144
21-23	D6S287	33	4	0.12	Breast	BJC 73:144
21-23	D6S287	22	4	0.18	Endocrine	CR 56:599
Unknown	D6S267	18	5	0.28	Ovary	GCC 15:223
22.3-23.1	ARG	12	2	0.17	Breast	BJC 73:144
22.3-23.1	ARG	15	0	0	Stomach	GCC 14:28
22.3-23.1	D6S262	28	10	0.36	Breast	BJC 73:144
Unknown	D6S262	35	12	0.34	Colon	CR 56:145
Unknown	D6S262	17	1	0.06	Head&Neck	CR 54:4756
Unknown	D6S262	21	3	0.14	Head&Neck	CR 54:4756
Unknown	D6S32	18	9	0.5	Stomach	GCC 14:28
23.1	D6S87	17	6	0.35	Ovary	BJC 69:429
23.1	D6S87	18	3	0.17	Ovary	CR 55:2169
23.1	D6S87	7	2	0.29	Ovary	CR 55:2169
23.1	D6S87	20	1	0.05	Uterus	CR 54:4294
22-23	MYB	10	0	0	Cervix	CR 49:3598
22-23	MYB	11	2	0.18	Colon	N 331:273
22-23	MYB	20	2	0.1	Colon	BJC 53:382
22-23	MYB	13	0	0	Liver	JJCR 81:108
22-23	MYB	18	3	0.17	Lung	PN 84:9252
22-23	MYB	7	3	0.43	Melanoma	CR 51:5449
22-23	MYB	5	0	0	Neuroblastoma	CR 49:1095
22-23	MYB	9	6	0.67	Ovary	BJC 67:551
22-23	MYB	4	1	0.25	Ovary	GO 55:245
22-23	MYB	8	1	0.12	Ovary	CR 50:2724
22-23	MYB	7	0	0	Prostate	G 11:530
22-23	MYB	20	6	0.3	Sarcoma	CR 52:2419
22-23	MYB	12	1	0.08	Stomach	GCC 14:28
22-23	MYB	13	0	0	Stomach	CR 48:2988
22-23	MYB	12	2	0.17	Stomach	CR 52:3099
22-23	MYB	7	1	0.14	Uterus	CR 51:5632
Unknown	D6S250	24	1	0.04	Ovary	CR 55:2169
Unknown	D6S250	10	3	0.3	Ovary	CR 55:2169
Unknown	D6S136	16	2	0.12	Kidney	CR 51:5817
Unknown	D6S136	3	0	0	Ovary	CR 52:5815
Unknown	D6S136	9	0	0	Ovary	CR 52:5815
Unknown	D6S441	11	1	0.09	Endocrine	CR 56:599
Unknown	D6S441	30	13	0.43	Ovary	GCC 15:223
24-27	ESR	16	0	0	Cervix	CGC 79:74
24-27	ESR	8	3	0.38	Colon	GCC 3:468
24-27	ESR	8	4	0.5	Melanoma	CR 51:5449

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24-27	ESR	23	6	0.26	Ovary	CR 55:2169
24-27	ESR	6	1	0.17	Ovary	CR 55:2169
24-27	ESR	13	2	0.15	Ovary	GO 47:137
24-27	ESR	14	9	0.64	Ovary	CR 50:2724
24-27	ESR	22	1	0.05	Ovary	TJC 54:546
24-27	ESR	15	10	0.67	Ovary	BJC 67:551
24-27	ESR	18	10	0.56	Ovary	GCC 15:223
24-27	ESR	1	1	1	Pancreas	GCC 3:468
24-27	ESR	6	0	0	Stomach	GCC 3:468
24-27	ESR	16	0	0	Stomach	CR 51:2926
24-27	ESR	6	1	0.17	Uterus	CR 51:5632
Unknown	D6S415	22	9	0.41	Ovary	GCC 15:223
25.2	D6S255	9	3	0.33	Breast	BJC 73:144
25.2	D6S255	23	2	0.09	Head&Neck	CR 54:1152
25.2	D6S255	7	3	0.43	Ovary	CR 55:2169
25.2	D6S255	11	2	0.18	Ovary	CR 55:2169
Unknown	D6S305	29	4	0.14	Cervix	CR 56:197
Unknown	D6S305	40	16	0.4	Colon	CR 56:145
Unknown	D6S305	15	2	0.13	Endocrine	CR 56:599
Unknown	D6S305	29	9	0.31	Melanoma	CR 56:589
Unknown	D6S305	35	13	0.37	Ovary	GCC 15:223
Unknown	IGF2R	16	11	0.69	Liver	O 10:1725
Unknown	IGF2R	2	0	0	Ovary	CR 55:2169
Unknown	IGF2R	4	1	0.25	Ovary	CR 55:2169
Unknown	IGF2R	18	5	0.28	Ovary	GCC 15:223
Unknown	IGF2R	11	3	0.27	Ovary	CR 55:2169
Unknown	IGF2R	7	0	0	Ovary	CR 55:2169
Unknown	IGF2R	18	2	0.11	Stomach	GCC 14:28
Unknown	IGF2R	10	2	0.2	Uterus	CR 54:4294
26-27	PLG	2	0	0	Liver	PNAS 86:8852
Unknown	D6S195	14	5	0.36	Ovary	CR 52:5815
Unknown	D6S195	2	0	0	Ovary	CR 52:5815
Unknown	D6S195	5	0	0	Ovary	CR 52:5815
Unknown	D6S191	16	3	0.19	Ovary	CR 52:5815
Unknown	D6S191	5	0	0	Ovary	CR 52:5815
Unknown	D6S191	8	0	0	Ovary	CR 52:5815
26	D6S186	25	5	0.2	Breast	BJC 71:290
26	D6S186	34	7	0.21	Kidney	CR 51:5817
26	D6S186	19	8	0.42	Ovary	CR 52:5815
26	D6S186	19	8	0.42	Ovary	GCC 15:223
26	D6S186	6	1	0.17	Ovary	CR 52:5815
26	D6S186	5	0	0	Ovary	CR 52:5815
Unknown	SOD2	11	3	0.27	Melanoma	CR 51:5449
Unknown	SOD2	8	4	0.5	Ovary	BJC 67:551
Unknown	SOD2	23	5	0.22	Stomach	GCC 14:28
Unknown	D6S264	32	13	0.41	Colon	CR 56:145

Chromosome 6 - q Arm

Unknown	D6S264	12	5	0.42	Endocrine	CR 56:599
Unknown	D6S264	15	5	0.33	Head&Neck	CR 54:1152
Unknown	D6S264	3	1	0.33	Kidney	GCC 12:76
Unknown	D6S264	34	12	0.35	Ovary	GCC 15:223
Unknown	D6S503	34	14	0.41	Colon	CR 56:145
21-qter	D6S2	8	3	0.38	Colon	GCC 3:468
21-qter	D6S2	19	4	0.21	Ovary	IJC 52:575
21-qter	D6S2	5	3	0.6	Ovary	O 5:219
21-qter	D6S2	21	1	0.05	Ovary	IJC 54:546
21-qter	D6S2	1	1	1	Pancreas	GCC 3:468
21-qter	D6S2	6	0	0	Stomach	GCC 3:468
Unknown	D6S133	22	14	0.64	Ovary	BJC 67:551
Unknown	D6S193	56	9	0.16	Esophageal	GCC 10:177
Unknown	D6S193	38	23	0.61	Ovary	GCC 15:223
27	D6S297	19	4	0.21	Breast	BJC 71:290
Unknown	D6S297	27	14	0.52	Ovary	GCC 15:223
Unknown	TCP10	17	12	0.71	Ovary	BJC 67:551
27	D6S44	56	4	0.07	Breast	CR 53:4356
27	D6S44	12	4	0.33	Breast	GCC 2:191
27	D6S44	29	4	0.14	Ovary	IJC 54:546
27	D6S44	18	0	0	Testis	NI 73:606
Unknown	D6S149	19	6	0.32	Ovary	GCC 15:223
Unknown	D6S149	8	2	0.25	Ovary	CR 52:5815
Unknown	D6S149	9	1	0.11	Ovary	CR 52:5815
Unknown	D6S149	22	10	0.45	Ovary	CR 52:5815
Unknown	D6S37	4	1	0.25	Breast	CR 53:3804
Unknown	D6S37	23	2	0.09	Breast	CR 50:7184
Unknown	D6S37	20	4	0.2	Cervix	CR 54:4481
Unknown	D6S37	5	2	0.4	Cervix	GCC 9:119
Unknown	D6S37	5	4	0.8	Endocrine	CR 56:599
Unknown	D6S37	13	2	0.15	Esophageal	CR 54:2996
Unknown	D6S37	13	4	0.31	Kidney	CR 51:820
Unknown	D6S37	25	9	0.36	Kidney	CR 51:5817
Unknown	D6S37	29	1	0.03	Lung	CR 52:2478
Unknown	D6S37	10	4	0.4	Melanoma	CR 51:5449
Unknown	D6S37	13	8	0.62	Ovary	BJC 67:551
Unknown	D6S37	29	5	0.17	Ovary	CR 51:5118
Unknown	D6S37	14	3	0.21	Sarcoma	CR 52:2419
Unknown	D6S37	30	11	0.37	Stomach	GCC 14:28
Unknown	D6S37	29	2	0.07	Testis	O 9:2245
Unknown	D6S37	11	1	0.09	Uterus	GCC 9:119
27	D6S446	24	11	0.46	Ovary	GCC 15:223
Unknown	D6S132	15	11	0.73	Ovary	BJC 67:551
27	D6S281	27	5	0.19	Breast	BJC 71:290
27	D6S281	39	13	0.33	Ovary	GCC 15:223
27	D6S281	39	13	0.33	Ovary	GCC 15:223

Chromosome 6 - q Arm

Unknown	Unknown	22	2	0.09	Brain	CR 50:5784
27	D6S193	29	8	0.28	Breast	BJC 71:290
25.2-27	D6S220	19	5	0.26	Breast	BJC 71:290
14-15	D6S330	12	6	0.5	Breast	BJC 71:290
23.3-25.2	D6S355	24	4	0.17	Breast	BJC 71:290
21-23.3	D6S357	20	2	0.1	Breast	BJC 71:290
21-23.3	D6S359	37	8	0.22	Breast	BJC 71:290
14-16	D6S39	1	1	1	Breast	CR 53:3804
16-21	D6S48	3	1	0.33	Breast	CR 53:3804
25.1	ER	47	9	0.19	Breast	BJC 71:448
24	D6S135	9	5	0.56	Kidney	CR 51:5817
21	D6S154	15	3	0.2	Kidney	CR 51:5817
27	D6S156	27	7	0.26	Kidney	CR 51:5817
23	D6S164	11	1	0.09	Kidney	CR 51:5817
Unknown	D6S281-D6S311-D6S278	22	4	0.18	Kidney	PNAS 92:2854
Unknown	D6S281-D6S311-D6S278	6	1	0.17	Kidney	PNAS 92:2854
Unknown	Unknown	20	15	0.75	Lung	CR 54:2322
12.0-21	CGA	13	3	0.23	Melanoma	CR 51:5449
Unknown	D6S29	4	0	0	Melanoma	CR 51:5449
27	Unknown	130	4	0.03	Ovary	IJC 52:575
Unknown	Unknown	23	1	0.04	Ovary	IJC 52:575
13	ACTBP2	21	7	0.33	Ovary	GO 55:245
Unknown	D6S125	17	4	0.24	Ovary	BJC 67:551
27	D6S193	10	1	0.1	Ovary	CR 52:5815
27	D6S193	11	1	0.09	Ovary	CR 52:5815
27	D6S193	23	11	0.48	Ovary	CR 52:5815
Unknown	D6S225	26	0	0	Ovary	CR 55:2169
Unknown	D6S225	13	2	0.15	Ovary	CR 55:2169
23.3-25.2	D6S355	6	0	0	Ovary	CR 55:2169
Unknown	D6S366	14	2	0.14	Ovary	CR 55:2169
Unknown	D6S366	19	1	0.05	Ovary	CR 55:2169
Unknown	D6S86	22	13	0.59	Ovary	BJC 67:551
Unknown	HCG-A	8	4	0.5	Ovary	BJC 67:551
Unknown	IGF2R-D6S:251-249	17	3	0.18	Ovary	BJC 72:1330
Unknown	MYB-DMDL-SOD2-D6S44	37	21	0.57	Ovary	CR 53:2393
27	Unknown	3	0	0	Pancreas	CR 54:2761
21.3	TNFB	13	2	0.15	Uterus	CR 54:4294
SUM		3960	978	0.25		

Chromosome 7 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
22	D7S21	36	5	0.14	Stomach	CR 51:2926
22	D7S21	19	1	0.05	Stomach	HG 92:244
22	D7S21	26	1	0.04	Testis	GCC 13:249
Unknown	D7S517	6	0	0	Kidney	PNAS 92:2854
Unknown	D7S517	21	0	0	Kidney	PNAS 92:2854
Unknown	D7S370	18	3	0.17	Brain	CR 50:5784
Unknown	D7S370	8	1	0.12	Breast	CR 50:7184
Unknown	D7S370	24	2	0.08	Cervix	CR 54:4481
Unknown	D7S370	24	5	0.21	Esophageal	CR 54:2996
Unknown	D7S370	10	2	0.2	Kidney	CR 51:820
Unknown	D7S370	10	0	0	Liver	CR 51:89
Unknown	D7S370	18	5	0.28	Lung	CR 52:2478
Unknown	D7S370	26	4	0.15	Ovary	IJC 54:546
Unknown	D7S370	2	2	1	Pancreas	CR 54:2761
Unknown	D7S370	23	1	0.04	Testis	O 9:2245
Unknown	D7S370	20	2	0.1	Esophageal	GCC 10:177
Unknown	D7S370	10	1	0.1	Esophageal	CR 51:2115
Unknown	D7S370	7	3	0.43	Ovary	CR 51:5118
Unknown	D7S370	17	2	0.12	Sarcoma	CR 52:2419
Unknown	D7S371	21	1	0.05	Breast	CR 53:4356
Unknown	D7S371	2	0	0	Ovary	CR 51:5118
13.0-12	EGFR	8	1	0.12	Cervix	CR 49:3598
13.0-12	EGFR	4	0	0	Liver	PNAS 86:8852
11.2-12	EGFR	18	3	0.17	Ovary	BJC 69:429
11.2-12	EGFR	14	0	0	Ovary	CR 49:1220
13.0-12	EGFR	5	1	0.2	Ovary	CR 50:2724
Unknown	EGFR	11	0	0	Ovary	CR 50:2724
13.0-12	EGFR	13	1	0.08	Prostate	G 11:530
Unknown	EGFR	10	0	0	Uterus	CR 51:5632
13.0-12	EGFR	16	2	0.12	Uterus	CR 54:4294
13.0-12	EGFR	16	2	0.12	Uterus	CR 54:4294
Unknown	D7S372	12	0	0	Brain	CR 49:6572
Unknown	D7S493	32	2	0.06	Cervix	CR 56:197
Unknown	D7S507	25	1	0.04	Cervix	CR 56:197
2.2-ter	Unknown	35	1	0.03	Colon	BJC 59:750
Unknown	D7S481	22	16	0.73	Colon	CR 56:145
Unknown	D7S507	20	1	0.05	Endocrine	CR 56:599
Unknown	D7S481	21	0	0	Head&Neck	CR 54:4756
Unknown	D7S481	22	4	0.18	Head&Neck	CR 54:4756
Unknown	D7S507	26	6	0.23	Head&Neck	CR 54:1152
pter-q22	Unknown	11	1	0.09	Liver	BJC 54:1083
pter-q22	Unknown	13	1	0.08	Liver	BJC 67:1007
Unknown	D7S481	30	1	0.03	Melanoma	CR 56:589
Unknown	D7S135	11	4	0.36	Ovary	CR 53:2393
pter-q22	Unknown	10	0	0	Pancreas	BJC 65:809
2.2-ter	Unknown	10	0	0	Stomach	BJC 59:750

Chromosome 7 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
21.3-22.1	COL1A2	29	1	0.03	Breast	GCC 2:191
21.3-22.1	COL1A2	6	0	0	Cervix	CR 49:3598
21.3-22.1	COL1A2	12	0	0	Colon	N 331:273
21.3-22.1	COL1A2	15	1	0.07	Liver	JJCR 81:108
21.3-22.1	COL1A2	11	0	0	Liver	CCG 48:72
21.3-22.1	COL1A2	5	0	0	Neuroblastom a	CR 49:1095
21.3-22.1	COL1A2	10	2	0.2	Stomach	CR 52:3099
21.3-22.1	COL1A2	6	0	0	Uterus	CR 51:5632
Unknown	D7S527	21	4	0.19	Breast	PNAS 91:12155
Unknown	D7S527	8	1	0.12	Colon	CR 55:1347
Unknown	D7S527	9	2	0.22	Head&Neck	CR 55:1347
Unknown	D7S527	8	1	0.12	Prostate	CR 54:6370
Unknown	D7S479	12	1	0.08	Breast	PNAS 91:12155
Unknown	D7S479	17	0	0	Endocrine	CR 56:599
Unknown	D7S518	27	6	0.22	Breast	PNAS 91:12155
Unknown	D7S518	8	0	0	Colon	CR 55:1347
Unknown	D7S518	13	2	0.15	Head&Neck	CR 55:1347
Unknown	D7S518	11	3	0.27	Prostate	CR 54:6370
Unknown	D7S515	13	3	0.23	Breast	PNAS 91:12155
Unknown	D7S496	17	8	0.47	Breast	PNAS 91:12155
Unknown	D7S496	13	4	0.31	Colon	CR 55:1347
Unknown	D7S496	10	1	0.1	Head&Neck	CR 55:1347
Unknown	D7S496	8	3	0.38	Prostate	CR 54:6370
22.3-31.2	D7S13	21	4	0.19	Breast	PNAS 91:12155
Unknown	D7S523	22	12	0.55	Breast	PNAS 91:12155
Unknown	D7S523	9	4	0.44	Colon	CR 55:1347
Unknown	D7S523	13	5	0.38	Head&Neck	CR 55:1347
Unknown	D7S523	7	2	0.29	Prostate	CR 54:6370
Unknown	D7S18	7	3	0.43	Breast	PNAS 91:12155
Unknown	D7S486	15	5	0.33	Breast	PNAS 91:12155
Unknown	D7S486	18	9	0.5	Colon	CR 55:1347
Unknown	D7S486	10	3	0.3	Head&Neck	CR 55:1347
Unknown	D7S486	6	2	0.33	Prostate	CR 54:6370
Unknown	D7S23	18	7	0.39	Breast	PNAS 91:12155
Unknown	D7S23	11	1	0.09	Ovary	BJC 69:429
Unknown	D7S23	15	2	0.13	Ovary	CR 53:2393
Unknown	D7S23	20	3	0.15	Uterus	CR 54:4294
31	MET	31	1	0.03	Breast	CR 53:4356
31	MET	121	49	0.4	Breast	L 339:140
31	MET	221	84	0.38	Breast	GCC 12:304
31	MET	18	8	0.44	Breast	PNAS 91:12155
31	MET	24	2	0.08	Breast	GCC 2:191
31	MET	15	0	0	Colon	CCG 48:167
31	MDR1-MET	12	0	0	Prostate	G 11:530
31	MET	9	3	0.33	Prostate	GCC 11:179

Chromosome 7 - q Arm

31	MET	14	1	0.07	Sarcoma	CR 52:2419
31	MET	35	7	0.2	Stomach	IJC 59:597
31	MET	1	0	0	Testis	CCG 52:72
31	MET	1	0	0	Testis	CCG 52:72
31	MET	1	0	0	Testis	CCG 52:72
Unknown	D7S633	7	4	0.57	Colon	CR 55:1347
Unknown	D7S633	6	2	0.33	Head&Neck	CR 55:1347
Unknown	D7S633	7	3	0.43	Prostate	CR 54:6370
Unknown	D7S677	9	6	0.67	Colon	CR 55:1347
Unknown	D7S677	10	4	0.4	Head&Neck	CR 55:1347
Unknown	D7S677	8	5	0.62	Prostate	CR 54:6370
Unknown	D7S655	8	4	0.5	Colon	CR 55:1347
Unknown	D7S655	7	3	0.43	Head&Neck	CR 55:1347
Unknown	D7S655	14	6	0.43	Prostate	CR 54:6370
Unknown	D7S522	11	9	0.82	Breast	PNAS 91:12155
Unknown	D7S522	10	8	0.8	Colon	CR 55:1347
Unknown	D7S522	15	8	0.53	Head&Neck	CR 55:1347
Unknown	D7S522	6	5	0.83	Prostate	CR 54:6370
Unknown	D7S480	21	9	0.43	Breast	PNAS 91:12155
Unknown	D7S480	27	4	0.15	Cervix	CR 56:197
Unknown	D7S480	16	7	0.44	Colon	CR 55:1347
Unknown	D7S480	10	4	0.4	Head&Neck	CR 55:1347
Unknown	D7S480	11	3	0.27	Prostate	CR 54:6370
Unknown	D7S487	15	4	0.27	Breast	PNAS 91:12155
Unknown	D7S487	8	2	0.25	Colon	CR 55:1347
Unknown	D7S487	10	0	0	Head&Neck	CR 55:1347
Unknown	D7S487	19	1	0.05	Leukemia	CR 55:5377
Unknown	D7S487	8	1	0.12	Prostate	CR 54:6370
31	CFTR	9	2	0.22	Ovary	BJC 69:429
Unknown	D7S490	14	5	0.36	Breast	PNAS 91:12155
Unknown	D7S490	10	4	0.4	Colon	CR 55:1347
Unknown	D7S490	12	4	0.33	Head&Neck	CR 55:1347
Unknown	D7S490	6	1	0.17	Prostate	CR 54:6370
31-32	D7S125	12	5	0.42	Breast	PNAS 91:12155
31-32	D7S125	15	2	0.13	Ovary	IJC 54:546
Unknown	D7S504	22	6	0.27	Breast	PNAS 91:12155
Unknown	D7S514	10	1	0.1	Breast	PNAS 91:12155
Unknown	D7S500	19	3	0.16	Breast	PNAS 91:12155
Unknown	D7S500	31	9	0.29	Cervix	CR 56:197
Unknown	D7S495	18	0	0	Breast	PNAS 91:12155
Unknown	D7S495	17	0	0	Head&Neck	CR 54:4756
Unknown	D7S495	20	1	0.05	Head&Neck	CR 54:4756
Unknown	D7S495	24	7	0.29	Head&Neck	CR 54:1152
Unknown	D7S495	26	1	0.04	Melanoma	CR 56:589
Unknown	D7S498	18	2	0.11	Breast	PNAS 91:12155
Unknown	D7S498	9	2	0.22	Colon	CR 55:1347

Chromosome 7 - q Arm

Unknown	D7S498	8	0	0	Head&Neck	CR 55:1347
Unknown	D7S498	4	0	0	Prostate	CR 54:6370
Unknown	D7S483	19	1	0.05	Breast	PNAS 91:12155
Unknown	D7S505	11	0	0	Breast	PNAS 91:12155
Unknown	D7S396	5	0	0	Brain	CR 49:6572
Unknown	D7S396	22	6	0.27	Breast	PNAS 91:12155
Unknown	D7S396	20	3	0.15	Breast	CR 50:7184
Unknown	D7S396	17	1	0.06	Esophageal	CR 54:2996
Unknown	D7S396	44	5	0.11	Esophageal	GCC 10:177
Unknown	D7S396	23	6	0.26	Kidney	CR 51:820
Unknown	D7S396	28	3	0.11	Liver	CR 51:89
Unknown	D7S396	34	5	0.15	Lung	CR 52:2478
Unknown	D7S396	19	4	0.21	Ovary	CR 51:5118
Unknown	D7S396	18	0	0	Sarcoma	CR 52:2419
36	D7S550	6	0	0	Colon	CR 55:1347
36	D7S550	28	3	0.11	Esophageal	IJC 69:1
36	D7S550	6	0	0	Head&Neck	CR 55:1347
36	D7S550	8	1	0.12	Prostate	CR 54:6370
36	D7S550	8	1	0.12	Prostate	CR 54:6370
Unknown	Unknown	31	0	0	Brain	CR 50:5784
Unknown	ABP1	6	2	0.33	Breast	PNAS 91:12155
32-qter	D7S228	18	2	0.11	Cervix	CR 54:4481
Unknown	D7S96	10	3	0.3	Cervix	GCC 9:119
3.3-ter	Unknown	32	0	0	Colon	BJC 59:750
Unknown	D7S368	21	0	0	Colon	CCG 48:167
Unknown	D7S22	11	0	0	Endocrine	N 328:524
Unknown	Unknown	10	0	0	Liver	BJC 64:1083
36	Unknown	12	0	0	Liver	BJC 67:1007
31.3-qter	Unknown	7	1	0.14	Pancreas	BJC 65:809
36	Unknown	4	0	0	Pancreas	CR 54:2761
31.3-qter	Unknown	19	2	0.11	Prostate	CSurveys 11:15
Unknown	Unknown	19	2	0.11	Prostate	PNAS 87:8731
3.3-ter	Unknown	9	0	0	Stomach	BJC 59:750
Unknown	D7S22	47	11	0.23	Stomach	IJC 59:597
Unknown	D7S22	41	10	0.24	Stomach	CR 51:2926
Unknown	D7S63	35	9	0.23	Stomach	IJC 59:597
Unknown	D7S64	16	0	0	Stomach	IJC 59:597
Unknown	D7S95	30	13	0.43	Stomach	IJC 59:597
Unknown	D7S22	22	2	0.09	Testis	GCC 13:249
32-qter	D7S228	23	2	0.09	Testis	O 9:2245
Unknown	TCBR	3	0	0	Testis	CCG 52:72
Unknown	TCBR	3	0	0	Testis	CCG 52:72
Unknown	TCBR	2	0	0	Testis	CCG 52:72
11.23	D7S440	19	1	0.05	Uterus	CR 54:4294
Unknown	D7S96	16	3	0.19	Uterus	GCC 9:119
SUM		2325	517	0.22		

Chromosome 7 - p Arm

SUM	747	87	0.12
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Chromosome 8 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
21	D8S17	21	7	0.33	Breast	CR 53:4356
21	D8S17	3	1	0.33	Breast	CR 53:3804
21	D8S17	9	1	0.11	Ovary	IJC 54:546
Unknown	D8S264	30	6	0.2	Cervix	CR 56:197
Unknown	D8S262	5	2	0.4	Kidney	GCC 12:76
Unknown	D8S262	15	2	0.13	Leukemia	CR 55:5377
Unknown	D8S262	18	9	0.5	Prostate	CR 54:6061
23	D8S201	9	5	0.56	Colon	AJP 144:1
23	D8S201	28	6	0.21	Prostate	O 11:2121
23	D8S201	15	8	0.53	Prostate	AJP 144:1
23	D8S201	22	3	0.14	Prostate	CR 53:3869
23	D8S201	3	1	0.33	Sarcoma	AJP 144:1
23	D8S7	11	5	0.45	Colon	GCC 10:1
23	D8S7	18	6	0.33	Esophageal	CR 54:2996
23	D8S7	10	4	0.4	Ovary	CR 53:2393
23	D8S7	8	3	0.38	Prostate	GCC 3:215
23	D8S7	6	3	0.5	Prostate	G 11:530
23	D8S7	10	1	0.1	Sarcoma	CR 52:2419
Unknown	D8S277	18	0	0	Endocrine	CR 56:599
Unknown	D8S277	26	11	0.42	Prostate	CR 54:6061
23.1-.2	D8S337	18	5	0.28	Colon	CR 53:1172
23.1-.2	D8S337	15	7	0.47	Liver	GCC 7:152
23.1-.2	D8S337	3	0	0	Lung	GCC 8:75
23.1-.2	D8S337	14	6	0.43	Prostate	GCC 13:168
23.1-.2	D8S336	39	10	0.26	Colon	CR 53:1172
23.1-.2	D8S336	48	18	0.38	Liver	GCC 7:152
23.1-.2	D8S336	7	3	0.43	Lung	GCC 8:75
21.3-22	D8S335	53	18	0.34	Colon	CR 53:1172
21.3-22	D8S335	30	15	0.5	Colon	GCC 10:7
21.3-22	D8S335	46	17	0.37	Liver	GCC 7:152
21.3-22	D8S335	18	4	0.22	Liver	GCC 10:7
21.3-22	D8S335	27	12	0.44	Lung	GCC 10:7
21.3-22	D8S335	5	1	0.2	Lung	GCC 7:85
Unknown	D8S265	22	5	0.23	Cervix	CR 56:197
Unknown	D8S265	22	11	0.5	Prostate	CR 54:6061
22	CTSB	33	14	0.42	Colon	CR 53:1172
22	CTSB	23	7	0.3	Liver	GCC 7:152
11.21-.2	Unknown	33	10	0.3	Colon	CR 52:5368
11.21-.2	Unknown	34	8	0.24	Colon	CR 53:1172
11.21-.2	Unknown	34	0	0	Liver	GCC 7:152
11.21-.2	Unknown	12	0	0	Lung	GCC 7:85
Unknown	D8S254	13	4	0.31	Breast	CR 55:4995
Unknown	D8S261	16	1	0.06	Head&Neck	CR 54:4756
Unknown	D8S261	18	1	0.06	Head&Neck	CR 54:4756
Unknown	D8S261	20	8	0.4	Head&Neck	CR 54:1152
Unknown	D8S261	6	3	0.5	Kidney	GCC 12:76

Chromosome 8 - p Arm

Unknown	D8S261	24	3	0.12	Melanoma	CR 56:589
Unknown	D8S261	31	17	0.55	Prostate	CR 54:6061
22-pter	D8S163	44	19	0.43	Colon	CR 53:1172
22-pter	D8S163	31	14	0.45	Liver	GCC 7:152
22-pter	D8S163	14	3	0.21	Lung	GCC 8:75
22-pter	D8S163	1	0	0	Pancreas	CR 54:2761
22-pter	D8S163	23	14	0.61	Prostate	CR 53:3869
22-pter	D8S163	18	9	0.5	Prostate	GCC 13:168
21.3-22	CI8-I344	71	25	0.35	Colon	GCC 10:7
21.3-22	CI8-I344	40	10	0.25	Liver	GCC 10:7
21.3-22	CI8-I344	30	8	0.27	Lung	GCC 10:7
21.3-22	CI8-2195	35	15	0.43	Colon	GCC 10:7
21.3-22	CI8-2195	32	7	0.22	Liver	GCC 10:7
21.3-22	CI8-2195	20	6	0.3	Lung	GCC 10:7
21.3-22	CI8-2014	24	7	0.29	Colon	GCC 10:7
21.3-22	CI8-2014	6	2	0.33	Liver	GCC 10:7
21.3-22	CI8-2014	17	7	0.41	Lung	GCC 10:7
21.3-22	CI8-2014	8	3	0.38	Prostate	GCC 13:168
21.3-22	D8S233	21	10	0.48	Colon	GCC 10:7
21.3-22	D8S233	24	11	0.46	Colon	CR 53:1172
21.3-22	D8S233	28	12	0.43	Liver	GCC 7:152
21.3-22	D8S233	14	5	0.36	Liver	GCC 10:7
21.3-22	D8S233	9	2	0.22	Lung	GCC 8:75
21.3-22	D8S233	7	3	0.43	Lung	GCC 10:7
Unknown	MSR	56	5	0.09	Breast	CR 52:5368
21.3-22	MSR	74	27	0.36	Colon	GCC 10:7
Unknown	MSR	26	12	0.46	Colon	CR 52:5368
22	MSR	74	28	0.38	Colon	CR 53:1172
Unknown	MSR	27	2	0.07	Kidney	CR 52:5368
Unknown	MSR	33	14	0.42	Liver	JJCR 84:893
22	MSR	87	37	0.43	Liver	GCC 7:152
21.3-22	MSR	54	10	0.19	Liver	GCC 10:7
Unknown	MSR	35	14	0.4	Lung	CR 52:5368
Unknown	MSR	21	9	0.43	Lung	GCC 8:75
21.3-22	MSR	38	16	0.42	Lung	GCC 10:7
Unknown	MSR	12	4	0.33	Ovary	CR 52:5368
21.3-22	MSR	29	18	0.62	Prostate	GCC 13:168
22	MSR	29	20	0.69	Prostate	CR 53:3869
Unknown	MSR	18	4	0.22	Stomach	CR 52:5368
21.3-22	Unknown	33	16	0.48	Colon	GCC 10:7
21.3-22	Unknown	9	3	0.33	Liver	GCC 10:7
21.3-22	Unknown	20	12	0.6	Lung	GCC 10:7
21.3-22	Unknown	18	11	0.61	Prostate	GCC 13:168
21.3-22	Unknown	21	9	0.43	Colon	GCC 10:7
21.3-22	Unknown	6	2	0.33	Liver	GCC 10:7
21.3-22	Unknown	22	15	0.68	Lung	GCC 10:7

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21.3-22	Unknown	12	19	0.45	Colon	GCC 10:7
21.3-22	Unknown	33	10	0.3	Liver	GCC 10:7
21.3-22	Unknown	21	10	0.48	Lung	GCC 10:7
21.3-22	Unknown	15	8	0.53	Prostate	GCC 13:168
21.3-22	Unknown	48	14	0.29	Colon	GCC 10:7
21.3-22	Unknown	39	9	0.23	Liver	GCC 10:7
21.3-22	Unknown	22	7	0.32	Lung	GCC 10:7
21.3-22	Unknown	15	8	0.53	Prostate	GCC 13:168
21.3-22	Unknown	49	22	0.45	Colon	GCC 10:7
21.3-22	Unknown	40	9	0.23	Liver	GCC 10:7
21.3-22	Unknown	23	7	0.3	Lung	GCC 10:7
21.3-22	Unknown	15	8	0.53	Prostate	GCC 13:168
21.3-22	Unknown	51	31	0.61	Colon	GCC 10:7
21.3-22	Unknown	54	16	0.3	Liver	GCC 10:7
21.3-22	Unknown	24	5	0.21	Lung	GCC 10:7
21.3-22	Unknown	20	8	0.4	Colon	GCC 10:7
21.3-22	Unknown	25	7	0.28	Liver	GCC 10:7
21.3-22	Unknown	17	4	0.24	Lung	GCC 10:7
21	Unknown	1	0	0	Pancreas	CR 54:2761
22	LPL	10	4	0.4	Colon	GCC 11:195
22	LPL	13	2	0.15	Colon	AJP 144:1
22	LPL	32	4	0.12	Colon	GCC 10:1
22	LPL	21	3	0.14	Colon	CR 53:1172
22	LPL	47	10	0.21	Colon	BJC 70:18
22	LPL	17	4	0.24	Leukemia	B 83:3449
22	LPL	38	19	0.5	Liver	GCC 7:152
22	LPL	6	4	0.67	Lung	CR 55:28
22	LPL	7	3	0.43	Lung	GCC 8:75
22	LPL	19	8	0.42	Prostate	AJP 144:1
22	LPL	13	5	0.38	Prostate	GCC 13:278
22	LPL	7	6	0.86	Prostate	GCC 3:215
22	LPL	32	15	0.47	Prostate	CR 53:3869
22	LPL	24	11	0.46	Prostate	O 11:2121
p22	LPL-G214-15	29	14	0.48	Prostate	CR 54:6061
22	LPL	2	0	0	Sarcoma	AJP 144:1
22	LPL	19	2	0.11	Uterus	CR 54:4294
Unknown	D8S258	16	3	0.19	Breast	CR 55:4995
Unknown	D8S282	27	13	0.48	Prostate	CR 54:6061
Unknown	D8S298	30	18	0.6	Prostate	CR 54:6061
21.3	D8S232	59	17	0.29	Colon	CR 53:1172
21.3	D8S232	40	13	0.33	Liver	GCC 7:152
21.3	D8S232	19	7	0.37	Lung	GCC 7:85
21.3	D8S334	47	16	0.34	Colon	CR 53:1172
21.3-22	D8S334	49	18	0.37	Colon	GCC 10:7
21.3-22	D8S334	37	8	0.22	Liver	GCC 10:7
21.3	D8S334	39	15	0.38	Liver	GCC 7:152

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21.3-22	D8S334	19	8	0.42	Lung	GCC 10:7
21.3	D8S334	6	2	0.33	Lung	GCC 7:85
21.3	D8S334	16	9	0.56	Prostate	GCC 13:168
21-23	EGR3	28	14	0.5	Colon	CR 53:1172
21-23	EGR3	33	12	0.36	Liver	GCC 7:152
21.2-.3	C18-586	25	7	0.28	Colon	CR 53:1172
21.2-.3	C18-586	20	9	0.45	Liver	GCC 7:152
21	D8S133	10	5	0.5	Prostate	GCC 11:119
21	D8S133	27	7	0.26	Prostate	O 11:2121
21	D8S133	29	16	0.55	Prostate	CR 54:6061
21.2-.3	D8S220	50	18	0.36	Colon	CR 53:1172
21.2-.3	D8S220	35	13	0.37	Colon	CR 52:5368
21.2-.3	D8S220	43	16	0.37	Liver	CR 52:5368
21.2-.3	D8S220	50	17	0.34	Liver	GCC 7:152
21.2-.3	D8S220	17	4	0.24	Lung	GCC 7:85
21.2-.3	D8S220	18	6	0.33	Prostate	GCC 13:168
21.2-.3	D8S220	27	16	0.59	Prostate	CR 53:3869
Unknown	SFTP2	40	11	0.28	Colon	GCC 10:1
Unknown	D8S136	20	7	0.35	Breast	CR 55:4995
Unknown	D8S136	11	6	0.55	Colon	GCC 11:195
Unknown	D8S136	1	1	1	Prostate	AJP 144:1
Unknown	D8S136	28	16	0.57	Prostate	CR 54:6061
21.1-.2	D8S221	53	14	0.26	Colon	CR 53:1172
21.1-.2	D8S221	41	10	0.24	Liver	GCC 7:152
21.1-.2	D8S221	10	0	0	Lung	GCC 7:85
21	NEFL	15	1	0.07	Brain	CR 50:5784
21	NEFL	2	1	0.5	Breast	CR 53:3804
21	NEFL	22	3	0.14	Cervix	CR 54:4481
21	NEFL	35	11	0.31	Colon	GCC 10:1
21	NEFL	8	4	0.5	Colon	GCC 11:195
21	NEFL	50	22	0.44	Colon	CR 53:1172
21	NEFL	47	19	0.4	Liver	GCC 7:152
21	NEFL	14	5	0.36	Lung	GCC 7:85
21	NEFL	6	2	0.33	Prostate	CR 53:3869
21	NEFL	8	7	0.88	Prostate	GCC 3:215
21	NEFL	19	8	0.42	Prostate	GCC 13:168
21	NEFL	21	9	0.43	Prostate	O 11:2121
21	NEFL	19	3	0.16	Testis	O 9:2245
Unknown	D8S137	16	10	0.62	Breast	CR 55:4995
Unknown	D8S137	85	29	0.34	Colon	BJC 70:18
Unknown	D8S137	1	1	1	Prostate	AJP 144:1
Unknown	D8S137	23	16	0.7	Prostate	CR 54:6061
Unknown	D8S137	2	2	1	Sarcoma	AJP 144:1
Unknown	D8S283	28	11	0.39	Prostate	CR 54:6061
p12	D8S87	14	2	0.14	Colon	AJP 144:1
p12	D8S87	24	9	0.38	Prostate	CR 54:6061

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p12	D8S87	20	5	0.25	Prostate	O 11:2121
p12	D8S87	18	4	0.22	Prostate	AJP 144:1
p12	D8S87	4	4	1	Sarcoma	AJP 144:1
p12	D8S87	25	5	0.2	Uterus	CR 54:4294
Unknown	D8S255	28	10	0.36	Prostate	CR 54:6061
Unknown	D8S255	10	1	0.1	Testis	LI 73:606
11.2	ANK1	78	18	0.23	Colon	BJC 70:18
11.2	ANK1	7	4	0.57	Prostate	AJP 144:1
11.2	ANK1	1	0	0	Sarcoma	AJP 144:1
11.21-.22	D8S194	40	6	0.15	Colon	CR 52:5368
11.21-.22	D8S194	40	5	0.12	Colon	CR 53:1172
11.21-.22	D8S194	45	5	0.11	Liver	CR 52:5368
11.21-.22	D8S194	45	5	0.11	Liver	GCC 7:152
11.21-.22	D8S194	26	3	0.12	Prostate	CR 53:3869
11.22-.23	D8S234	58	13	0.22	Colon	CR 53:1172
11.22-.23	D8S234	57	14	0.25	Liver	GCC 7:152
11.22-.23	D8S234	13	3	0.23	Lung	GCC 7:85
11.22-.23	D8S234	15	2	0.13	Prostate	GCC 13:168
23.2-.3	D8S140	33	6	0.18	Colon	CR 52:5368
23.2-.3	D8S140	29	8	0.28	Colon	CR 53:1172
23.2-.3	D8S140	39	7	0.18	Liver	GCC 7:152
23.2-.3	D8S140	39	7	0.18	Liver	CR 52:5368
23.2-.3	D8S140	38	4	0.11	Prostate	CR 53:3869
11.0-12	POLB	15	0	0	Colon	GCC 10:1
12-11.2	PLAT	7	2	0.29	Prostate	GCC 3:215
12-11.2	PLAT	18	0	0	Prostate	O 11:2121
11.23	D8S223	24	0	0	Colon	CR 53:1172
11.23	D8S223	37	0	0	Liver	GCC 7:152
11.23	D8S223	37	0	0	Liver	GCC 7:152
Unknown	D8S262-261	26	17	0.65	Bladder	CR 55:5213
Unknown	D8S2	5	2	0.4	Breast	CR 53:3804
Unknown	D8S26	27	1	0.04	Breast	CR 53:4356
Unknown	D8S349	18	10	0.56	Breast	CR 55:4995
Unknown	D8S264-D8S265-D8S560	22	4	0.18	Kidney	PNAS 92:2854
Unknown	D8S264-D8S265-D8S560	6	1	0.17	Kidney	PNAS 92:2854
Unknown	D8S238	37	7	0.19	Liver	CR 52:5368
21	ARDRA3	19	5	0.26	Ovary	IJC 54:546
Unknown	D8S339	28	10	0.36	Prostate	CR 54:6061
22-21.3	D8S360	11	5	0.45	Prostate	O 11:2121
Unknown	D8S18	18	0	0	Testis	G 5:134
SUM		5603	1838	0.33		

Chromosome 8 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D8S260	28	7	0.25	Prostate	CR 54:6061
q22	D8S167	35	4	0.11	Prostate	CR 54:6061
Unknown	D8S257	16	0	0	Head&Neck	CR 54:4756
Unknown	D8S257	20	8	0.4	Head&Neck	CR 54:1152
Unknown	D8S257	14	0	0	Head&Neck	CR 54:4756
Unknown	D8S257	6	3	0.5	Kidney	GCC 12:76
Unknown	D8S257	26	2	0.08	Melanoma	CR 56:589
Unknown	D8S257	31	17	0.55	Prostate	CR 54:6061
Unknown	D8S273	30	6	0.2	Cervix	CR 56:197
Unknown	D8S273	19	3	0.16	Head&Neck	CR 54:1152
Unknown	D8S284	21	5	0.24	Cervix	CR 56:197
24	TG	2	0	0	Neuroblastom a	CR 49:1095
24	TG	14	4	0.29	Ovary	CR 53:2393
24	TG	9	0	0	Prostate	G 11:530
24	TG	8	0	0	Prostate	GCC 3:215
24	D8S39	14	1	0.07	Breast	CR 50:7184
24	D8S39	14	0	0	Cervix	CR 54:4481
24	D8S39	5	0	0	Cervix	GCC 9:119
24	D8S39	9	0	0	Esophageal	CR 51:2113
24	D8S39	22	0	0	Esophageal	CR 54:2996
24	D8S39	12	1	0.08	Kidney	CR 51:820
24	D8S39	20	4	0.2	Liver	CR 51:89
24	D8S39	1	1	1	Lung	CR 52:2478
24	D8S39	3	1	0.33	Lung	CR 52:2478
24	D8S39	8	1	0.12	Lung	CR 52:2478
24	D8S39	1	1	1	Lung	CR 52:2478
24	D8S39	16	5	0.31	Ovary	CR 51:5118
24	D8S39	7	0	0	Prostate	GCC 3:215
24	D8S39	17	2	0.12	Prostate	CR 53:3869
24	D8S39	14	1	0.07	Sarcoma	CR 52:2419
24	D8S39	18	4	0.22	Testis	O 9:2245
24	D8S39	8	0	0	Uterus	GCC 9:119
24	D8S39	8	0	0	Uterus	GCC 9:119
Unknown	Unknown	25	0	0	Brain	CR 50:5784
22-23	Unknown	2	0	0	Cervix	BJC 67:71
Unknown	D8S272	15	0	0	Endocrine	CR 56:599
Unknown	D8S177	42	4	0.1	Esophageal	GCC 10:177
Unknown	D8S272-D8S284	6	0	0	Kidney	PNAS 92:2854
Unknown	D8S272-D8S284	21	1	0.05	Kidney	PNAS 92:2854
Unknown	D8S:272-281	21	2	0.1	Leukemia	CR 55:5377
22-QTER	D8S161	19	5	0.26	Ovary	BJC 69:429
Unknown	D8S198	22	1	0.05	Uterus	CR 54:4294
Unknown	D8S84	20	0	0	Uterus	CR 54:4294
SUM		661	94	0.14		

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Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D9S143	33	17	0.52	Ovary	BJC 73:420
Unknown	D9S129	33	18	0.55	Ovary	BJC 73:420
22-24	D9S54	61	11	0.18	Bladder	CR 54:2848
22-PTER	D9S54	10	3	0.3	Ovary	BJC 69:429
Unknown	D9S132	5	1	0.2	Ovary	O 11:1249
Unknown	D9S132	3	0	0	Ovary	O 11:1249
Unknown	D9S199	21	15	0.71	Head&Neck	CR 54:1152
Unknown	D9S199	10	0	0	Ovary	O 11:1249
Unknown	D9S199	12	2	0.17	Ovary	O 11:1249
Unknown	D9S199	33	17	0.52	Ovary	BJC 73:420
Unknown	D9S124	23	2	0.09	Ovary	CR 55:2150
Unknown	D9S144	12	1	0.08	Ovary	O 11:1249
Unknown	D9S144	8	3	0.38	Ovary	O 11:1249
22	IFNA	40	26	0.65	Bladder	CR 54:2848
22	IFNA	12	1	0.08	Brain	CR 54:1397
22	IFNA	19	4	0.21	Brain	CR 54:1397
22	IFNA	89	21	0.24	Breast	IJC 64:378
Unknown	IFNA	13	4	0.31	Esophageal	CL 97:129
22	IFNA	2	0	0	Kidney	GCC 12:76
Unknown	IFNA	40	8	0.2	Kidney	JJCR 86:795
Unknown	IFNA	6	5	0.83	Lung	CR 55:28
Unknown	IFNA	15	8	0.53	Ovary	GO 55:245
Unknown	IFNA	28	3	0.11	Ovary	CR 55:2150
Unknown	IFNA	33	19	0.58	Ovary	BJC 73:420
22	IFNA	58	20	0.34	Ovary	AJHG 55:143
Unknown	IFNA	7	0	0	Ovary	O 11:1249
Unknown	IFNA	3	0	0	Ovary	O 11:1249
22	IFNA	19	5	0.26	Stomach	CR 55:1933
Unknown	IFNB	252	153	0.61	Bladder	CR 53:1230
22	IFNB1	252	153	0.61	Bladder	CR 53:1230
Unknown	IFNB	6	0	0	Breast	CR 53:4356
22	IFNB1	1	0	0	Breast	GCC 2:191
22	IFNB1	12	1	0.08	Cervix	CR 54:4481
22	IFNB1	42	5	0.12	Leukemia	AHEM 68:171
22	IFNB1	44	0	0	Leukemia	AHEM 68:171
22	IFNB1	6	0	0	Prostate	G 11:530
22	IFNB1	7	5	0.71	Testis	O 9:2245
Unknown	D9S156	126	30	0.24	Breast	IJC 64:378
Unknown	D9S156	11	4	0.36	Esophageal	CL 97:129
Unknown	D9S156	18	13	0.72	Head&Neck	CR 54:1152
Unknown	D9S156	3	0	0	Ovary	O 11:1249
Unknown	D9S156	13	4	0.31	Ovary	O 11:1249
21	D9S157	133	30	0.23	Breast	IJC 64:378
21	D9S157	30	5	0.17	Cervix	CR 56:197
21	D9S157	13	6	0.46	Esophageal	CL 97:129
21	D9S157	65	25	0.38	Esophageal	IJC 69:1

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21	D9S157	5	1	0.2	Kidney	GCC 12:76
Unknown	D9S168	120	17	0.14	Breast	IJC 64:378
Unknown	D9S168	33	15	0.45	Ovary	BJC 73:420
21	CDKN2	109	20	0.18	Bladder	JNCI 87:1524
21	p15-p16	50	28	0.56	Esophageal	HMG 4:1883
21	CDKN2	55	1	0.02	Kidney	JJCR 86:795
21	CDKN2	34	7	0.21	Lung	GCC 14:164
21	CDKN2	50	24	0.48	Ovary	IJC 63:222
21	p15-p16	56	3	0.05	Sarcoma	CGC 86:136
21	MTS2	100	18	0.18	Bladder	JNCI 87:1524
21	D9S162	90	10	0.11	Breast	IJC 64:378
21	D9S162	9	3	0.33	Esophageal	CL 97:129
21	D9S162	33	4	0.12	Head&Neck	CR 54:4756
21	D9S162	41	13	0.32	Head&Neck	CR 54:4756
21	D9S162	4	0	0	Kidney	GCC 12:76
21	D9S162	33	17	0.52	Ovary	BJC 73:420
21	D9S162	12	1	0.08	Ovary	O 11:1249
21	D9S162	15	3	0.2	Ovary	O 11:1249
21	D9S171	139	28	0.2	Breast	IJC 64:378
21	D9S171	60	19	0.32	Esophageal	IJC 69:1
21	D9S171	11	4	0.36	Esophageal	CL 97:129
21	D9S171	3	0	0	Kidney	GCC 12:76
21	D9S171	12	3	0.25	Kidney	JJCR 86:795
Unknown	D9S:162-171	6	3	0.5	Kidney	GCC 12:76
21	D9S171	24	4	0.17	Lung	GCC 14:164
21	D9S171	8	5	0.62	Lung	CR 54:2307
Unknown	D9S:162-171	35	16	0.46	Melanoma	CR 56:589
21	D9S171	9	3	0.33	Ovary	O 11:1249
21	D9S171	33	16	0.48	Ovary	BJC 73:420
21	D9S171	15	1	0.07	Ovary	O 11:1249
Unknown	D9S126	252	152	0.6	Bladder	CR 53:1230
Unknown	D9S126	252	152	0.6	Bladder	CR 53:1230
Unknown	D9S126	80	15	0.19	Breast	IJC 64:378
Unknown	D9S126	16	3	0.19	Endocrine	CR 56:599
Unknown	IFN2a- D9S126	5	5	1	Lung	CR 55:513
Unknown	D9S126	9	0	0	Ovary	O 11:1249
Unknown	D9S126	11	1	0.09	Ovary	O 11:1249
Unknown	D9S126	51	17	0.33	Ovary	AJHG 55:143
Unknown	D9S126	30	3	0.1	Ovary	CR 55:2150
Unknown	D9S126	33	17	0.52	Ovary	BJC 73:420
Unknown	D9S736	33	18	0.55	Ovary	BJC 73:420
Unknown	D9S3	252	154	0.61	Bladder	CR 53:1230
21	D9S3	16	3	0.19	Bladder	CR 54:2848
21	D9S3	4	1	0.25	Breast	CR 53:3804
21	D9S169	22	4	0.18	Cervix	CR 56:197
21	D9S169	8	6	0.75	Lung	CR 54:2307

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21	S161	15	5	0.33	Esophageal	CL 97:129
21	S161	5	1	0.2	Kidney	GCC 12:76
21	S161	10	2	0.2	Ovary	O 11:1249
21	S161	14	0	0	Ovary	O 11:1249
Unknown	D9S104	117	20	0.17	Breast	IJC 64:378
Unknown	D9S104	63	27	0.43	Esophageal	IJC 69:1
Unknown	D9S104	33	15	0.45	Ovary	BJC 73:420
Unknown	D9S104	19	4	0.21	Uterus	CR 54:4294
21-qter	D9S52	12	5	0.42	Ovary	GO 55:245
Unknown	D9S165	4	0	0	Ovary	O 11:1249
Unknown	D9S165	8	0	0	Ovary	O 11:1249
Unknown	D9S200	11	2	0.18	Esophageal	CL 97:129
Unknown	D9S200	25	13	0.52	Head&Neck	CR 54:1152
Unknown	D9S200	33	13	0.39	Ovary	BJC 73:420
Unknown	D9S200	13	1	0.08	Ovary	O 11:1249
Unknown	D9S200	13	4	0.31	Ovary	O 11:1249
12	D9S55	14	1	0.07	Brain	CR 54:1397
12	D9S55	18	2	0.11	Brain	CR 54:1397
12	D9S55	18	2	0.11	Brain	CR 54:1397
Unknown	D9S47	252	152	0.6	Bladder	CR 53:1230
Unknown	IFNa- D9S1751- 736-1747-1748- 1752-171	31	19	0.61	Bladder	CR 55:5213
Unknown	Unknown	12	0	0	Brain	CR 50:5784
Unknown	D9S18	30	17	0.57	Esophageal	GCC 10:177
Unknown	MTS1	5	5	1	Esophageal	O 9:3737
Unknown	D9S168-D9S166	5	2	0.4	Kidney	PNAS 92:2854
Unknown	D9S168-D9S166	19	3	0.16	Kidney	PNAS 92:2854
Unknown	D9S168-171	50	20	0.4	Leukemia	CR 55:5377
Unknown	Unknown	33	17	0.52	Lung	CR 54:2322
Unknown	D9S171-D9S126- D9S169	29	17	0.59	Lung	JCRCO 121:291
Unknown	D9S171-D9S126- D9S169	6	0	0	Lung	JCRCO 121:291
Unknown	D9S171-D9S126- D9S169	47	10	0.21	Lung	JCRCO 121:291
Unknown	OVC	15	5	0.33	Ovary	CR 53:2393
SUM		4921	1868	0.38		

Chromosome 9 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D9S15	70	37	0.53	Bladder	O 11:1671
Unknown	D9S15	11	1	0.09	Breast	CR 50:7184
13-21.1	D9S15	6	3	0.5	Cervix	GCC 9:119
13-21.1	D9S15	14	1	0.07	Esophageal	CR 54:2996
Unknown	D9S15	22	9	0.41	Esophageal	GCC 10:177
Unknown	D9S15	12	2	0.17	Kidney	CR 51:820
13-21.1	D9S15	6	1	0.17	Kidney	GCC 12:76
Unknown	D9S15	8	1	0.12	Lung	CR 52:2478
13-21.1	D9S15	14	5	0.36	Ovary	BJC 69:429
Unknown	D9S15	4	0	0	Ovary	CR 51:5118
Unknown	D9S15	16	2	0.12	Ovary	CR 55:2150
Unknown	D9S15	33	15	0.45	Ovary	BJC 73:420
Unknown	D9S15	10	3	0.3	Sarcoma	CR 52:2419
13-21.1	D9S15	10	2	0.2	Uterus	GCC 9:119
Unknown	D9S18	252	151	0.6	Bladder	CR 53:1230
Unknown	D9S18	7	0	0	Cervix	GCC 5:119
Unknown	D9S18	28	10	0.36	Esophageal	CR 54:2996
Unknown	D9S18	13	4	0.31	Ovary	IJC 54:546
Unknown	D9S18	16	1	0.06	Uterus	GCC 9:119
Unknown	D9S27	8	2	0.25	Testis	O 9:2245
Unknown	D9S103	70	36	0.51	Bladder	O 11:1671
Unknown	D9S103	33	16	0.48	Ovary	BJC 73:420
Unknown	D9S166	8	2	0.25	Ovary	O 11:1249
Unknown	D9S166	3	0	0	Ovary	O 11:1249
Unknown	ASSP3	252	155	0.62	Bladder	CR 53:1230
Unknown	ASSP3	8	0	0	Liver	CCG 48:72
11-22.0	ASSP3	19	7	0.37	Ovary	BJC 69:429
11-22.0	ASSP3	8	0	0	Stomach	CR 48:2988
Unknown	S153	70	37	0.53	Bladder	O 11:1671
pter-q11	D9S1	2	0	0	Cervix	CR 49:3598
pter-q11	D9S1	13	1	0.08	Colon	IJC 53:382
pter-q11	D9S1	7	0	0	Liver	JJCR 81:108
pter-q11	D9S1	5	0	0	Neuroblastoma	CR 49:1095
pter-q11	D9S1	1	0	0	Pancreas	CR 54:2761
pter-q11	D9S1	14	1	0.07	Stomach	CR 52:3099
pter-q11	D9S1	6	0	0	Uterus	CR 51:5632
Unknown	D9S167	70	38	0.54	Bladder	O 11:1671
Unknown	D9S201	70	36	0.51	Bladder	O 11:1671
Unknown	D9S201	26	7	0.27	Ovary	CR 55:2150
Unknown	D9S201	33	13	0.39	Ovary	BJC 73:420
Unknown	D9S283	70	37	0.53	Bladder	O 11:1671
Unknown	D9S283	33	13	0.39	Ovary	BJC 73:420
Unknown	D9S12	70	36	0.51	Bladder	O 11:1671
Unknown	D9S12	9	0	0	Colon	CCG 48:167
Unknown	D9S12	33	12	0.36	Ovary	BJC 73:420

Chromosome 9 - q Arm

Unknown	D9S12	13	6	0.46	Ovary	CR 55:2150
Unknown	D9S119	70	38	0.54	Bladder	O 11:1671
Unknown	D9S197	6	3	0.5	Kidney	GCC 12:76
Unknown	D9S197	26	5	0.19	Melanoma	CR 56:589
Unknown	D9S22	252	154	0.61	Bladder	CR 53:1230
Unknown	D9S176	70	38	0.54	Bladder	O 11:1671
Unknown	D9S176	6	1	0.17	Kidney	GCC 12:76
Unknown	D9S29	4	1	0.25	Head&Neck	CL 79:67
Unknown	D9S29	19	11	0.58	Ovary	CR 55:2150
Unknown	D9S109	70	37	0.53	Bladder	O 11:1671
Unknown	D9S109	5	1	0.2	Kidney	GCC 12:76
Unknown	D9S109	29	6	0.21	Ovary	CR 55:2150
Unknown	D9S127	70	36	0.51	Bladder	O 11:1671
Unknown	D9S127	24	7	0.29	Ovary	CR 55:2150
Unknown	D9S127	33	18	0.55	Ovary	BJC 73:420
Unknown	D9S53	70	38	0.54	Bladder	O 11:1671
Unknown	D9S53	19	3	0.16	Head&Neck	CR 54:1152
Unknown	D9S53	35	12	0.34	Ovary	CR 55:2150
Unknown	D9S53	33	19	0.58	Ovary	BJC 73:420
Unknown	D9S53	24	1	0.04	Uterus	CR 54:4294
Unknown	D9S58	70	37	0.53	Bladder	O 11:1671
Unknown	D9S58	27	7	0.26	Ovary	CR 55:2150
Unknown	D9S105	70	37	0.53	Bladder	O 11:1671
Unknown	HXB	70	39	0.56	Bladder	O 11:1671
Unknown	HXB	33	17	0.52	Ovary	BJC 73:420
Unknown	HXB	24	10	0.42	Ovary	CR 55:2150
Unknown	HXB	19	1	0.05	Uterus	CR 54:4294
Unknown	D9S155	33	15	0.45	Ovary	BJC 73:420
Unknown	D9S16	12	6	0.5	Ovary	CR 55:2150
Unknown	D9S59	70	37	0.53	Bladder	O 11:1671
Unknown	D9S59	33	18	0.55	Ovary	BJC 73:420
Unknown	D9S59	30	10	0.33	Ovary	CR 55:2150
Unknown	D9S154	70	38	0.54	Bladder	O 11:1671
Unknown	D9S154	34	5	0.15	Cervix	CR 56:197
Unknown	D9S302	36	4	0.11	Brain	CR 55:4696
Unknown	D9S302	36	4	0.11	Brain	CR 55:4696
Unknown	D9S258	70	35	0.5	Bladder	O 11:1671
33	GSN	70	39	0.56	Bladder	O 11:1671
33	GSN	17	3	0.18	Head&Neck	CR 54:1152
33	GSN	5	0	0	Kidney	GCC 12:76
33	GSN	18	8	0.44	Ovary	BJC 69:429
Unknown	GSN	33	16	0.48	Ovary	BJC 73:420
33	GSN	15	7	0.47	Ovary	CR 55:2150
Unknown	D9S49	252	154	0.61	Bladder	CR 53:1230
31-34	D9S28	39	5	0.13	Bladder	CR 54:2848
31-34	D9S28	1	1	1	Head&Neck	CL 79:67

Chromosome 9 - q Arm

Unknown	D9S60	70	36	0.51	Bladder	O 11:1671
Unknown	D9S61	70	38	0.54	Bladder	O 11:1671
34-QTER	D9S64	17	8	0.47	Ovary	BJC 69:429
Unknown	D9S64	18	10	0.56	Ovary	CR 55:2150
34.1	ABL	65	13	0.2	Bladder	CR 54:2848
34.1	ABL	70	37	0.53	Bladder	O 11:1671
34.1	ABL	33	15	0.45	Ovary	BJC 73:420
34.1	ABL	25	10	0.4	Ovary	CR 55:2150
34-qter	ASS	20	5	0.25	Bladder	CR 54:2848
34-qter	ASS	17	0	0	Brain	CR 54:1397
34-qter	ASS	12	0	0	Brain	CR 54:1397
34-qter	ASS	14	2	0.14	Lung	PN 84:9252
34-qter	ASS	34	13	0.38	Ovary	CR 55:2150
Unknown	D9S164	6	1	0.17	Kidney	PNAS 92:2854
Unknown	D9S164	20	3	0.15	Kidney	PNAS 92:2854
Unknown	D9S10	252	154	0.61	Bladder	CR 53:1230
34.3	D9S10	41	13	0.32	Bladder	CR 54:2848
34.3	D9S10	15	8	0.53	Ovary	CR 55:2150
Unknown	D9S66	70	38	0.54	Bladder	O 11:1671
Unknown	D9S14	252	151	0.6	Bladder	CR 53:1230
Unknown	D9S67	70	36	0.51	Bladder	O 11:1671
Unknown	D9S13	252	151	0.6	Bladder	CR 53:1230
34	D9S17	35	6	0.17	Breast	CR 50:7184
34	D9S17	21	16	0.16	Esophageal	GCC 10:177
34	D9S17	31	8	0.26	Lung	CR 52:2478
34	D9S17	20	2	0.1	Ovary	CR 51:5118
Unknown	D9S7	252	155	0.62	Bladder	CR 53:1230
34	D9S7	65	13	0.2	Bladder	CR 54:2848
34	D9S7	7	0	0	Brain	CR 49:6572
34	D9S7	21	2	0.1	Breast	GCC 2:191
Unknown	D9S7	44	6	0.14	Breast	CR 53:4356
34	D9S7	5	1	0.2	Breast	CR 53:3804
34	D9S7	3	2	0.67	Cervix	GCC 9:119
34	D9S7	33	5	0.15	Cervix	CR 54:4481
34	D9S7	20	1	0.05	Endocrine	GCC 13:9
Unknown	D9S7	9	0	0	Esophageal	CR 51:2113
34	D9S7	24	7	0.29	Esophageal	CR 54:2996
34	D9S7	10	1	0.1	Kidney	CR 51:820
34	D9S7	9	0	0	Liver	CR 51:89
34	D9S7	6	1	0.17	Liver	BJC 64:1083
34	D9S7	11	1	0.09	Liver	BJC 67:1007
Unknown	D9S7	32	6	0.19	Ovary	IJC 54:546
34	D9S7	6	1	0.17	Ovary	CR 55:2150
34	D9S7	2	0	0	Pancreas	CR 54:2761
34	D9S7	13	1	0.08	Pancreas	BJC 65:809
34	D9S7	12	0	0	Prostate	G 11:530

Chromosome 9 - q Arm

34	D9S7	13	2	0.15	Prostate	CSurveys 11:15
34	D9S7	11	2	0.18	Sarcoma	CR 52:2419
Unknown	D9S7	19	1	0.05	Testis	GCC 13:249
Unknown	D9S7	33	16	0.48	Testis	O 9:2245
34	D9S7	5	1	0.2	Uterus	GCC 9:119
Unknown	D9S11	252	153	0.61	Bladder	CR 53:1230
34	D9S7-D9S11-D9S13	252	149	0.59	Bladder	O 8:1083
34	D9S7-D9S11-D9S13	252	149	0.59	Bladder	O 8:1083
Unknown	GSN-D9S:15-12	28	17	0.61	Bladder	CR 55:5213
Unknown	Unknown	20	1	0.05	Brain	CR 50:5384
21.1-22.2	Unknown	14	1	0.07	Brain	CR 54:1397
21.1-22.2	Unknown	19	0	0	Brain	CR 54:1397
Unknown	D9S6	13	0	0	Colon	CCG 48:167
Unknown	D9S146	9	1	0.11	Endocrine	CR 56:599
Unknown	D9S160-180	44	26	0.59	Head&Neck	CR 54:4756
Unknown	D9S160-180	39	2	0.05	Head&Neck	CR 54:4756
Unknown	D9S:154-164-180	52	10	0.19	Leukemia	CR 55:5377
Unknown	Unknown	33	16	0.48	Lung	CR 54:2322
Unknown	D9S15-10	26	14	0.54	Ovary	CR 53:2393
Unknown	Unknown	19	2	0.11	Prostate	PNAS 87:8751
SUM		6593	3076	0.47		

Chromosome 10 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
pter-p11.2	D10S89	17	0	0	Uterus	CR 54:4294
Unknown	Unknown	38	15	0.39	Brain	CR 50:5784
Unknown	D10S109	7	0	0	Brain	CR 53:2386
Unknown	D10S109	6	2	0.33	Brain	CR 53:2386
11.2	D10S111	9	0	0	Brain	CR 53:2386
11.2	D10S111	6	0	0	Brain	CR 53:2386
pter-p11.2	D10S89	8	0	0	Brain	CR 54:1397
pter-p11.2	D10S89	16	1	0.06	Brain	CR 54:1397
pter-p11.2	D10S89	6	1	0.17	Brain	CR 53:2386
pter-p11.2	D10S89	13	0	0	Brain	CR 54:1397
Unknown	FNRB-D10S28	72	31	0.43	Brain	CR 56:164
pter-q13	D10 S28	32	4	0.12	Breast	CR 50:7184
Unknown	D10S15	15	0	0	Breast	GCC 2:191
pter-q13	D10 S28	42	9	0.21	Cervix	CR 54:4481
Unknown	D10S191	32	1	0.03	Cervix	CR 56:197
13-12.2	D10S24	4	0	0	Cervix	CR 54:4481
Unknown	D10S28	7	1	0.14	Cervix	GCC 9:119
Unknown	D10S249	14	1	0.07	Endocrine	CR 56:599
pter-p11.2	D10S89	20	1	0.05	Endocrine	GCC 13:9
pter-q13	D10S17	33	11	0.33	Esophageal	GCC 10:177
pter-q13	D10S17	14	2	0.14	Esophageal	CR 54:2996
Unknown	D10S226	11	0	0	Head&Neck	CR 54:4756
Unknown	D10S226	12	0	0	Head&Neck	CR 54:4756
Unknown	D10S249	22	5	0.23	Head&Neck	CR 54:1152
pter-q13	D10 S28	31	3	0.1	Kidney	CR 51:5817
pter-q13	D10 S28	34	3	0.09	Kidney	CR 51:820
pter-q13	D10S17	11	1	0.09	Kidney	CR 51:5817
Unknown	D10S226	6	3	0.5	Kidney	GCC 12:76
Unknown	D10S249-D10S191	21	0	0	Kidney	PNAS 92:285
Unknown	D10S249-D10S191	5	0	0	Kidney	PNAS 92:285
pter-q13	D10 S28	39	0	0	Liver	CR 51:89
pter-q13	D10 S28	35	5	0.14	Lung	CR 52:2478
11-23.0	D10S14	8	4	0.5	Melanoma	GCC 8:178
Unknown	D10S15	5	3	0.6	Melanoma	GCC 8:178
Unknown	D10S226	23	4	0.17	Melanoma	CR 56:589
Unknown	D10S28	14	5	0.36	Melanoma	GCC 8:178
Unknown	D10S33	3	0	0	Melanoma	GCC 8:178
pter-p11.2	D10S89	10	4	0.4	Melanoma	GCC 8:178
pter-q13	D10 S28	27	3	0.11	Ovary	CR 51:5118
pter-q13	D10 S28	35	5	0.14	Ovary	IJC 54:546
Unknown	D10S13-28	33	4	0.12	Ovary	CR 53:2393
pter-q13	D10 S28	7	3	0.43	Pancreas	CR 54:2761
pter-q13	D10 S28	19	4	0.21	Prostate	BJU 73:390
11-23.0	D10S14	11	3	0.27	Prostate	GCC 3:215
13-pter	D10S17	18	0	0	Prostate	CSurveys 11

Chromosome 10 - p Arm

pTER-p13	D10S17	11	6	0.55	Prostate	G 11:530
pter-p12	D10S17	11	6	0.55	Prostate	GCC 3:215
pTER-p13	D10S17	18	0	0	Prostate	PNAS 87:875
13-12.2	D10S24	14	4	0.29	Prostate	GCC 3:215
pter-p12	D10S17	14	5	0.36	Sarcoma	CR 52:2419
pter-q13	D10 S28	47	5	0.11	Testis	O 9:2245
Unknown	D10S28	14	4	0.29	Uterus	GCC 9:119
pter-p11.2	D10S89	17	0	0	Uterus	CR 54:4294
SUM		980	172	0.18		

Chromosome 10 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
24-TER	PLAU	5	0	0	Uterus	CR 51:5632
Unknown	Unknown	37	14	0.38	Brain	CR 50:5784
12-qter	Unknown	12	0	0	Brain	CR 54:1397
11.2	Unknown	12	0	0	Brain	CR 54:1397
11.2	Unknown	17	2	0.12	Brain	CR 54:1397
12-qter	Unknown	15	1	0.07	Brain	CR 54:1397
Unknown	D10S25-22-1	64	21	0.33	Brain	CR 56:164
22-23	D10S1	5	0	0	Brain	CR 48:5546
22-23	D10S1	4	0	0	Brain	CR 48:5546
22-23	D10S1	10	10	1	Brain	CR 48:5546
Unknown	D10S169	7	0	0	Brain	CR 53:2386
Unknown	D10S169	5	2	0.4	Brain	CR 53:2386
22-23	D10S4	21	20	0.95	Brain	CR 48:5546
22-23	D10S4	6	0	0	Brain	CR 48:5546
22-23	D10S4	11	0	0	Brain	CR 48:5546
24-TER	PLAU	10	0	0	Brain	CR 48:5546
24-TER	PLAU	5	0	0	Brain	CR 48:5546
24-TER	PLAU	14	14	1	Brain	CR 48:5546
22-23	D10S1	18	2	0.11	Breast	CR 53:4356
26	D10S25	6	2	0.33	Breast	CR 53:3804
26	D10S25	23	2	0.09	Breast	CR 50:7184
26	D10S25	30	5	0.17	Breast	GCC 2:191
22-23	D10S4	18	4	0.22	Breast	GCC 2:191
Unknown	D10S205	32	4	0.12	Cervix	CR 56:197
26	D10S25	32	9	0.28	Cervix	CR 54:4481
26	D10S25	8	2	0.25	Cervix	GCC 9:119
11	D10S30	8	2	0.25	Cervix	GCC 9:119
21.1	D10S5	17	1	0.06	Cervix	CR 54:4481
24-TER	PLAU	4	1	0.25	Cervix	CR 49:3598
24-TER	PLAU	6	0	0	Colon	IJC 53:382
Unknown	D10S187	22	2	0.09	Endocrine	CR 56:599
26	D10S25	25	4	0.16	Esophageal	CR 54:2996
26	D10S25	36	6	0.17	Esophageal	GCC 10:177
26	D10S25	17	0	0	Esophageal	CR 51:2113
Unknown	D10S185	12	3	0.25	Head&Neck	CR 54:4756
Unknown	D10S185	21	0	0	Head&Neck	CR 54:4756
Unknown	D10S221	24	5	0.21	Head&Neck	CR 54:1152
22-25	D10S13	32	9	0.28	Kidney	CR 51:5817
21	D10S14	17	5	0.29	Kidney	CR 51:5817
Unknown	D10S185	6	3	0.5	Kidney	GCC 12:76
21-TER	D10S20	25	8	0.32	Kidney	CR 51:5817
Unknown	D10S212-D10S190	19	1	0.05	Kidney	PNAS 92:2854
Unknown	D10S212-D10S190	5	0	0	Kidney	PNAS 92:2854
21	D10S22	10	3	0.3	Kidney	CR 51:5817
21	D10S23	15	3	0.2	Kidney	CR 51:5817
26	D10S25	30	10	0.33	Kidney	CR 51:5817

Chromosome 10 - q Arm

26	D10S25	21	6	0.29	Kidney	CR 51:820
22-25	D10S27	26	3	0.12	Kidney	CR 51:5817
11	D10S30	13	2	0.15	Kidney	CR 51:5817
26	D10S36	27	5	0.19	Kidney	CR 51:5817
Unknown	D10S201	19	1	0.05	Leukemia	CR 55:5377
Unknown	Unknown	16	0	0	Liver	CR 51:89
22-23	D10S1	3	1	0.33	Liver	CCG 48:72
26	D10S25	24	6	0.25	Liver	CR 51:89
Unknown	D10S26	24	6	0.25	Liver	CR 51:89
24-TER	PLAU	20	0	0	Liver	JJCR 81:108
26	D10S25	25	5	0.2	Lung	CR 52:2478
Unknown	ATC	9	4	0.44	Melanoma	CR 54:3111
Unknown	CHDC, GGA2F11	14	6	0.43	Melanoma	CR 54:3111
Unknown	D10S108	5	1	0.2	Melanoma	CR 54:3111
Unknown	D10S110	4	2	0.5	Melanoma	CR 54:3111
Unknown	D10S168	8	5	0.62	Melanoma	CR 54:3111
Unknown	D10S169	8	1	0.12	Melanoma	CR 54:3111
Unknown	D10S185	29	9	0.31	Melanoma	CR 56:589
Unknown	D10S187	12	3	0.25	Melanoma	CR 54:3111
21-22	D10S19	8	3	0.38	Melanoma	GCC 8:178
21-TER	D10S20	4	3	0.75	Melanoma	GCC 8:178
Unknown	D10S221	12	4	0.33	Melanoma	CR 54:3111
26	D10S36	9	4	0.44	Melanoma	GCC 8:178
Unknown	D10S610	9	4	0.44	Melanoma	CR 54:3111
Unknown	D10S88	6	3	0.5	Melanoma	CR 54:3111
24-TER	PLAU	5	0	0	Neuroblastom a	CR 49:1095
Unknown	D10S1-20	19	2	0.11	Ovary	CR 53:2393
Unknown	D10S173	16	3	0.19	Ovary	BJC 69:429
26	D10S25	34	4	0.12	Ovary	IJC 54:546
26	D10S25	24	5	0.21	Ovary	CR 51:5118
26	D10S25	4	0	0	Pancreas	CR 54:2761
Unknown	Unknown	24	7	0.29	Prostate	CSurveys 11:15
22-23	D10S1	2	0	0	Prostate	GCC 3:215
21-22	D10S19	8	1	0.12	Prostate	GCC 3:215
21-22	D10S19	7	0	0	Prostate	GCC 11:119
21-TER	D10S20	8	2	0.25	Prostate	GCC 3:215
26	D10S25	8	3	0.38	Prostate	GCC 11:119
26	D10S25	13	4	0.31	Prostate	G 11:530
26	D10S25	13	4	0.31	Prostate	GCC 3:215
Unknown	D10S26	9	2	0.22	Prostate	GCC 3:215
22-23	D10S4	10	1	0.1	Prostate	GCC 3:215
26	D10S90	19	8	0.42	Prostate	BJU 73:390
26	OAT	25	7	0.28	Prostate	PNAS 87:8751
24-TER	PLAU	9	2	0.22	Prostate	GCC 3:215
26	D10S25	17	9	0.53	Sarcoma	CR 52:2419
Unknown	Unknown	2	0	0	Stomach	CR 48:2988

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Unknown	D10S26	20	0	0	Stomach	CR 51:2926
26	D10S25	34	9	0.26	Testis	O 9:2245
11.2	PTC	1	0	0	Testis	CCG 52:72
11.2	PTC	2	1	0.5	Testis	CCG 52:72
11.2	PTC	1	0	0	Testis	CCG 52:72
Unknown	D10S173	16	1	0.06	Uterus	CR 54:4294
26	D10S25	14	6	0.43	Uterus	GCC 9:119
11	D10S30	12	3	0.25	Uterus	GCC 9:119
24-TER	PLAU	5	0	0	Uterus	CR 51:5632
SUM		1509	351	0.23		

Chromosome 11 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	HRAS1-D11S12	17	7	0.41	Bladder	CR 51:5405
15.5	HRAS	7	2	0.29	Brain	CR 49:6572
15.5	HRAS	30	3	0.1	Breast	GCC 4:113
15.5	HRAS	24	3	0.12	Breast	CR 53:4486
15.5	HRAS	5	0	0	Breast	GCC 2:191
15.5	HRAS	68	21	0.31	Breast	GCC 12:304
15.5	HRAS	30	8	0.27	Breast	IJC 53:11
15.5	HRAS	29	5	0.17	Breast	JJCR 84:11
15.5	HRAS	7	1	0.14	Breast	CR 53:3804
15.5	HRAS	33	1	0.03	Breast	CR 53:4356
15.5	HRAS	37	7	0.19	Breast	GP 5:554
15.5	HRAS	6	0	0	Cervix	CR 49:3598
15.5	HRAS	18	6	0.33	Cervix	PNAS 91:69
15.5	HRAS	15	1	0.07	Cervix	BJC 67:71
15.5	HRAS	10	0	0	Colon	N 331:273
15.5	HRAS	16	0	0	Colon	CCG 48:167
15.5	HRAS	9	0	0	Colon	N 331:273
15.5	HRAS	9	1	0.11	Esophageal	CR 51:2113
15.5	HRAS	21	4	0.19	Esophageal	GCC 10:177
15.5	HRAS	20	8	0.4	Esophageal	CR 54:2996
15.5	HRAS	12	1	0.08	Head&Neck	CR 52:1494
15.5	HRAS	3	0	0	Kidney	CMB 38:59
15.5	HRAS	14	1	0.07	Kidney	CR 51:1071
15.5	HRAS	5	0	0	Kidney	CMB 38:59
15.5	HRAS	13	4	0.31	Leukemia	B 75:819
15.5	HRAS	5	0	0	Liver	JJCR 81:10
15.5	HRAS	3	0	0	Liver	BJC 67:100
15.5	HRAS	13	0	0	Liver	GCC 1:312
15.5	HRAS	4	0	0	Liver	PNAS 86:88
15.5	HRAS	10	5	0.5	Liver	CCG 48:72
15.5	HRAS	5	0	0	Liver	BJC 64:108
15.5	HRAS	47	7	0.15	Lung	GCC 10:183
15.5	HRAS	39	7	0.18	Lung	CR 54:1145
15.5	HRAS	13	5	0.38	Lung	PN 86:5099
15.5	HRAS	13	6	0.46	Lung	PN 91:5513
15.5	HRAS	2	1	0.5	Lung	PN 91:5513
15.5	HRAS	12	6	0.5	Lung	PN 86:5099
15.5	HRAS	7	1	0.14	Lung	NEJ 317:11
15.5	HRAS	5	2	0.4	Lung	PN 86:5099
15.5	HRAS	13	3	0.23	Lung	PN 84:9252
15.5	HRAS	6	2	0.33	Lung	PN 91:5513
15.5	HRAS	4	0	0	Neuroblastom a	CR 49:1095
15.5	HRAS	25	10	0.4	Ovary	GO 47:137
15.5	HRAS	15	4	0.27	Ovary	GO 55:245
15.5	HRAS	11	5	0.45	Ovary	CR 50:2724

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15.5	HRAS	11	2	0.18	Ovary	IJC 54:546
15.5	HRAS	27	12	0.44	Ovary	C 72:2423
15.5	HRAS	10	5	0.5	Ovary	CR 49:1220
15.5	HRAS	13	2	0.15	Ovary	BJC 67:268
15.5	HRAS	19	9	0.47	Ovary	BRJ 66:103
15.5	HRAS	5	2	0.4	Pancreas	BJC 65:809
15.5	HRAS	20	7	0.35	Pediatric	CR 50:3279
15.5	HRAS	15	5	0.33	Pediatric	BG 97:163
15.5	HRAS	9	0	0	Prostate	GCC 11:119
15.5	HRAS	11	5	0.45	Sarcoma	CR 52:2419
15.5	HRAS	11	5	0.45	Sarcoma	CR 52:2419
15.5	HRAS	9	0	0	Stomach	CR 48:2988
15.5	HRAS	28	1	0.04	Stomach	CR 51:2926
15.5	HRAS	19	7	0.37	Stomach	HG 92:244
15.5	HRAS	6	0	0	Stomach	HG 89:445
15.5	HRAS	15	7	0.47	Testis	GCC 9:153
15.5	HRAS	5	2	0.4	Testis	CCG 52:72
15.5	HRAS	12	3	0.25	Testis	GCC 9:153
15.5	HRAS	13	5	0.38	Testis	G 5:134
15.5	HRAS	17	3	0.16	Testis	JU 153:168
15.5	HRAS	15	0	0	Testis	GCC 13:249
15.5	HRAS	13	5	0.33	Testis	GCC 7:85
15.5	HRAS	3	1	0.33	Testis	CCG 52:72
15.5	HRAS	3	1	0.33	Testis	CCG 52:72
15.5	HRAS	9	1	0.11	Uterus	CR 51:5632
15.5	IGF2	7	2	0.29	Bladder	HG 91:455
15.5	IGF2	15	1	0.07	Breast	GE 5:554
15.5	IGF2	13	3	0.23	Cervix	O 12:423
15.5	IGF2	1	0	0	Lung	PN 91:5513
15.5	IGF2	7	0	0	Lung	PN 91:5513
15.5	IGF2	1	0	0	Lung	PN 91:5513
15.5	IGF2	14	6	0.43	Ovary	BRJ 66:103
15.5	IGF2	9	6	0.67	Testis	JU 153:168
15.5	MUC2	17	2	0.12	Testis	GCC 13:249
15.5	H19	14	2	0.14	Cervix	O 12:423
Unknown	D11S922	46	8	0.17	Head&Neck	CR 54:4756
Unknown	D11S922	40	1	0.03	Head&Neck	CR 54:4756
Unknown	D11S922	6	1	0.17	Kidney	PNAS 92:28
Unknown	D11S922	19	1	0.05	Kidney	PNAS 92:28
Unknown	D11S922	8	4	0.5	Pediatric	HG 97:163
Unknown	D11S922	49	16	0.33	Stomach	CR 56:268
Unknown	D11S1318	16	7	0.44	Pediatric	HG 97:163
Unknown	D11S1318	15	9	0.6	Stomach	CR 56:268
15.5	INS	31	3	0.1	Breast	CR 50:7184
15.5	INS	23	4	0.17	Breast	GCC 2:191
15.5	INS	31	3	0.1	Breast	CR 50:7184

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15.5	INS	3	0	0	Cervix	CR 49:3598
15.5	INS	3	0	0	Cervix	CR 49:3598
15.5	INS	15	3	0.2	Colon	IJC 53:382
15.5	INS	15	3	0.2	Colon	IJC 53:382
15.5	INS	8	2	0.25	Endocrine	CR 51:1154
15.5	INS	22	5	0.23	Kidney	CR 51:820
15.5	INS	7	0	0	Kidney	CMB 38:59
15.5	INS	21	3	0.14	Kidney	CR 51:1031
15.5	INS	7	0	0	Kidney	CMB 38:59
15.5	INS	22	5	0.23	Kidney	CR 51:820
15.5	INS	6	0	0	Liver	GCC 1:312
15.5	INS	6	1	0.17	Liver	CR 51:456
15.5	INS	9	0	0	Liver	JJCR 81:10
15.5	INS	11	3	0.27	Liver	CR 51:898
15.5	INS	10	2	0.2	Liver	CCG 48:72
15.5	INS	10	3	0.3	Lung	PN 86:5099
15.5	INS	5	1	0.2	Lung	PN 86:5099
15.5	INS	14	7	0.5	Lung	PN 86:5099
15.5	INS	33	12	0.36	Lung	GCC 10:183
15.5	INS	8	1	0.12	Lung	PN 91:5513
15.5	INS	2	0	0	Lung	PN 91:5513
15.5	INS	8	1	0.12	Lung	PN 91:5513
15.5	INS	12	3	0.25	Lung	PN 84:9252
15.5	INS	6	0	0	Neuroblastom	CR 49:1095
15.5	INS	5	0	0	Ovary	CR 50:2724
15.5	INS	13	7	0.54	Ovary	GO 55:245
15.5	INS	32	12	0.38	Ovary	C 72:2423
15.5	INS	27	7	0.26	Ovary	CR 51:5116
15.5	INS	20	7	0.35	Ovary	BRJ 66:103
15.5	INS	23	10	0.43	Pediatric	CR 50:3279
15.5	INS	9	0	0	Stomach	CR 48:2988
15.5	INS	2	0	0	Stomach	CR 52:3099
15.5	INS	15	4	0.27	Testis	GCC 7:96
15.5	INS	5	1	0.2	Testis	CCG 52:72
15.5	INS	2	0	0	Testis	CCG 52:72
15.5	INS	5	2	0.4	Testis	CCG 52:72
15.5	INS	15	3	0.2	Testis	G 5:134
15.5	INS	18	3	0.17	Testis	GCC 13:249
15.5	INS	3	0	0	Uterus	CR 51:5632
15.5	TH	15	1	0.07	Brain	CR 54:1397
15.5	TH	21	3	0.14	Brain	CR 54:1397
15.5	TH	16	4	0.25	Breast	HMG 4:1889
15.5	TH	14	4	0.29	Breast	CR 54:6270
15.5	TH	41	11	0.27	Breast	CR 53:4486
15.5	TH	14	1	0.07	Cervix	BJC 67:71
15.5	TH	20	8	0.6	Cervix	PNAS 91:69

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15.5	TH	10	0	0	Kidney	CMB 38:59
15.5	TH	8	0	0	Kidney	CMB 38:59
15.5	TH	8	1	0.12	Lung	PN 91:5513
15.5	TH	10	0	0	Lung	PN 91:5513
15.5	TH	2	0	0	Lung	PN 91:5513
15.5	TH	20	7	0.35	Ovary	GC 45:247
15.5	TH	23	9	0.39	Pediatric	HG 97:163
15.5	DRD4	7	1	0.14	Lung	PN 91:5513
15.5	DRD4	3	0	0	Lung	PN 91:5513
Unknown	D11S454	13	8	0.46	Liver	CR 51:499
Unknown	D11S454	18	4	0.22	Lung	CR 52:2478
Unknown	D11S454	11	0	0	Ovary	CR 51:499
15.5	D11S988	1	0	0	Lung	PN 91:5513
15.5	D11S988	2	0	0	Lung	PN 91:5513
15.5	D11S988	17	6	0.35	Pediatric	HG 97:163
15.5	D11S988	17	12	0.71	Stomach	CR 56:252
15.5	D11S12	32	5	0.16	Breast	GE 5:554
15.5	D11S12	3	1	0.33	Breast	GCC 27:91
15.5	D11S12	0	0	0	Cervix	CR 49:3598
15.5	D11S12	12	5	0.42	Cervix	CR 54:4481
15.5	D11S12	33	6	0.18	Esophageal	CR 54:2996
15.5	D11S12	15	3	0.2	Kidney	CR 51:1071
15.5	D11S12	11	8	0.73	Lung	PN 91:5513
15.5	D11S12	1	1	1	Lung	PN 91:5513
15.5	D11S12	4	2	0.5	Lung	PN 91:5513
15.5	D11S12	4	2	0.5	Ovary	BRJ 66:103
15.5	D11S12	3	1	0.33	Stomach	HG 89:445
15.5	D11S12	1	1	1	Testis	CCG 52:72
15.5	D11S12	20	6	0.3	Testis	O 9:2245
15.5	D11S12	1	0	0	Testis	CCG 52:72
15.5	D11S12	8	3	0.38	Testis	JU 153:168
15.5	D11S12	5	1	0.2	Uterus	CR 51:5692
15.5-15.4	RRM1	42	7	0.17	Lung	GCC 10:183
15.5	HBB	27	9	0.33	Breast	CR 53:4486
15	HBB	6	0	0	Liver	PNAS 86:88
15.5	HBB	2	0	0	Lung	PN 91:5513
15.5	HBB	4	0	0	Lung	PN 91:5513
15.5	HBB	6	0	0	Lung	PN 91:5513
15.5	HBBG2	2	0	0	Lung	PN 86:5099
15.5	HBBG2	8	4	0.5	Lung	PN 86:5099
15.5	HBBG2	5	4	0.8	Lung	PN 86:5099
15.5	HBB	21	7	0.33	Pediatric	HG 97:163
15	GLOBIN	30	4	0.13	Breast	GE 5:554
15	GLOBIN	16	4	0.25	Ovary	BRJ 66:103
Unknown	GLOBIN	14	5	0.36	Ovary	BRJ 66:103
Unknown	GLOBIN	13	2	0.15	Ovary	BRJ 66:103

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15.5	D11S932	5	0	0	Lung	PN 91:5513
15.5	D11S932	9	1	0.11	Lung	PN 91:5513
15.5	D11S932	1	0	0	Lung	PN 91:5513
Unknown	D11S569	27	13	0.48	Stomach	CR 56:268
Unknown	D11S569	24	3	0.12	Uterus	CR 54:4294
pter-15.4	PTH	11	1	0.09	Bladder	HG 91:455
pter-15.4	PTH	15	1	0.07	Kidney	CR 51:1071
pter-15.4	PTH	7	0	0	Liver	GCC 1:312
pter-15.4	PTH	8	1	0.12	Liver	CCG 48:72
pter-15.4	PTH	7	1	0.14	Lung	PN 91:5513
pter-15.4	PTH	5	1	0.2	Lung	PN 91:5513
pter-15.4	PTH	29	9	0.31	Ovary	C 72:2423
pter-15.4	PTH	7	0	0	Testis	GCC 7:96
pter-15.4	PTH	3	2	0.67	Testis	CCG 52:72
pter-15.4	PTH	1	0	0	Testis	CCG 52:72
pter-15.4	PTH	1	0	0	Testis	CCG 52:72
pter-15.4	PTH	15	6	0.4	Testis	JU 153:168
13-15.1	D11S419	14	6	0.43	Ovary	BJC 69:429
Unknown	D11S902	28	8	0.29	Cervix	PNAS 91:69
14-qter	D11S899	23	4	0.17	Head&Neck	CR 54:1152
14-qter	D11S899	6	0	0	Kidney	GCC 12:76
15.5	D11S861	21	5	0.24	Endocrine	CR 56:599
15.5	D11S861	1	0	0	Lung	PN 91:5513
15.5	D11S861	9	0	0	Lung	PN 91:5513
15.5	D11S861	7	0	0	Lung	PN 91:5513
Unknown	D11S860	27	9	0.33	Breast	CR 53:4486
15.5	D11S860	36	10	0.28	Breast	Unknown
15.5	D11S860	36	10	0.28	Breast	CR 54:6270
15.5	D11S860	7	0	0	Lung	PN 91:5513
15.5	D11S860	7	0	0	Lung	PN 91:5513
15.5	D11S860	2	0	0	Lung	PN 91:5513
15.5	D11S860	5	0	0	Lung	PN 91:5513
15.5	D11S860	5	0	0	Lung	PN 91:5513
15.5	D11S860	2	0	0	Lung	PN 91:5513
15.5	D11S860	16	6	0.38	Pediatric	HG 97:163
15.5	D11S860	44	16	0.36	Stomach	CR 56:268
15.4	CALCA	6	0	0	Bladder	HG 91:455
15.4	CALCA	17	1	0.06	Breast	GCC 2:191
15.4	CALCA	22	0	0	Breast	GE 5:554
15.4	CALCA	10	3	0.3	Cervix	BJC 67:71
15.4	CALCA	5	0	0	Kidney	CMB 38:59
15.4	CALCA	4	0	0	Kidney	CMB 38:59
15.4	CALCA	7	0	0	Liver	CCG 48:72
15.4	CALCA	10	1	0.1	Liver	CR 51:4367
15.4	CALCA	3	0	0	Liver	GCC 1:312
15.4	CALCA	6	0	0	Lung	PN 86:5099

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15.4	CALCA	6	1	0.17	Lung	PN 91:5513
15.4	CALCA	6	2	0.33	Lung	PN 86:5099
15.4	CALCA	2	0	0	Lung	PN 86:5099
15.4	CALCA	3	1	0.33	Lung	PN 91:5513
15.4	CALCA	10	3	0.3	Ovary	C 72:2423
15.4	CALCA	15	6	0.4	Ovary	BRJ 66:103
15.4	CALCA	7	0	0	Stomach	HG 89:445
15.4	CALCA	6	3	0.5	Testis	GCC 7:96
Unknown	D11S929	33	3	0.09	Cervix	CR 56:197
Unknown	D11S929	17	4	0.24	Pediatric	HG 97:163
13	D11S323	3	1	0.33	Lung	PN 91:5513
13	D11S323	3	1	0.33	Lung	PN 91:5513
13	D11S907	16	3	0.19	Endocrine	CR 56:599
13	D11S907	14	1	0.07	Head&Neck	CR 54:1152
13	D11S907	1	0	0	Kidney	GCC 12:76
13	D11S16	17	4	0.24	Cervix	PNAS 91:69
13	D11S16	30	4	0.13	Colon	IJC 53:382
13	D11S16	5	0	0	Kidney	CMB 38:59
13	D11S16	4	0	0	Kidney	CMB 38:59
13	D11S16	6	0	0	Liver	GCC 1:312
13	D11S16	7	2	0.29	Lung	PN 91:5513
13	D11S16	1	1	1	Lung	PN 91:5513
13	D11S16	10	7	0.7	Lung	PN 91:5513
13	D11S16	25	2	0.08	Ovary	IJC 54:546
13	D11S16	23	6	0.26	Ovary	BRJ 66:103
13	D11S16	7	4	0.57	Testis	JU 153:168
13	D11S16	12	3	0.25	Testis	GCC 9:153
13	D11S16	12	5	0.42	Testis	GCC 7:96
13	D11S16	5	2	0.4	Testis	GCC 9:153
13	D11S16	13	1	0.08	Uterus	CR 51:5632
13	D11S151	4	0	0	Lung	PN 91:5513
13	D11S151	1	0	0	Lung	PN 91:5513
13	D11S151	3	0	0	Lung	PN 91:5513
13	D11S151	11	3	0.27	Pediatric	CR 50:3279
13	D11S151	1	0	0	Testis	GCC 9:153
13	D11S151	4	0	0	Testis	GCC 9:153
13	CAT	18	13	0.72	Bladder	HG 91:455
13	CAT	1	0	0	Kidney	CMB 38:59
13	CAT	16	2	0.12	Kidney	CR 51:1071
13	CAT	6	1	0.17	Kidney	CMB 38:59
13	CAT	7	0	0	Liver	CCG 48:72
13	CAT	9	0	0	Liver	GCC 1:312
13	CAT	8	3	0.38	Lung	PN 86:5099
13	CAT	2	0	0	Lung	PN 86:5099
13	CAT	40	6	0.15	Lung	GCC 10:183
13	CAT	7	1	0.14	Lung	PN 86:5099

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13	CAT	2	1	0.5	Lung	PN 91:5513
13	CAT	7	0	0	Lung	PN 91:5513
13	CAT	10	0	0	Ovary	IJC 54:546
13	CAT	24	6	0.25	Ovary	BRJ 66:103
13	CAT	14	2	0.14	Pediatric	CR 50:3279
13	CAT	4	1	0.25	Stomach	HG 89:445
13	CAT	12	5	0.42	Testis	JU 153:168
13	CAT	1	0	0	Testis	CCG 52:72
13	CAT	3	1	0.33	Testis	CCG 52:72
13	CAT	1	0	0	Testis	CCG 52:72
13	D11S325	3	0	0	Lung	PN 91:5513
13	D11S325	5	0	0	Lung	PN 91:5513
13	D11S325	6	2	0.33	Testis	GCC 9:153
13	D11S325	6	1	0.17	Testis	GCC 9:153
13	D11S325	16	2	0.12	Testis	GCC 7:96
13	D4S414	15	5	0.33	Bladder	HG 91:455
13	D4S414	2	1	0.5	Lung	CR 54:5643
13	D4S414	4	1	0.25	Lung	CR 54:5643
13	D4S414	21	4	0.19	Lung	CR 54:5643
13	B-FSH	16	6	0.38	Bladder	HG 91:455
13	B-FSH	4	0	0	Cervix	BJC 67:71
13	B-FSH	46	9	0.2	Lung	GCC 10:183
13	B-FSH	24	7	0.29	Ovary	BRJ 66:103
13	B-FSH	14	5	0.36	Pediatric	CR 50:3279
13	B-FSH	7	1	0.14	Stomach	HG 89:445
13	D11S905	25	0	0	Esophageal	IJC 69:1
13	D11S905	18	4	0.22	Pediatric	HG 97:163
11.2-12	D11S149	3	0	0	Endocrine	CR 51:1154
11.2-12	D11S149	7	1	0.14	Lung	PN 91:5513
11.2-12	D11S149	1	0	0	Lung	PN 91:5513
11.2-12	D11S149	5	0	0	Lung	PN 91:5513
12	D11S288	10	2	0.2	Cervix	PNAS 91:69
12	D11S1313	48	12	0.25	Lung	GCC 13:40
12	D11S1313	48	12	0.25	Lung	GCC 13:40
Unknown	D11S:907-929	28	15	0.54	Bladder	CR 55:5213
Unknown	Unknown	14	3	0.21	Brain	CR 50:5784
15	Unknown	35	2	0.06	Breast	JNCI 84:50
Unknown	D11SS1318	18	6	0.33	Breast	HMG 4:1889
Unknown	D11SS1323	9	5	0.56	Breast	HMG 4:1889
Unknown	D11SS1338	9	5	0.56	Breast	HMG 4:1889
Unknown	D11SS1760	7	2	0.29	Breast	HMG 4:1889
11	D11S554	22	5	0.23	Cervix	BJC 71:814
Unknown	D11S740	5	0	0	Cervix	GCC 9:119
11	D11S554	22	6	0.27	Endocrine	CR 56:599
15.5	D11S576	25	0	0	Kidney	BJC 69:230
Unknown	D11S:922-904	6	3	0.5	Kidney	GCC 12:76

Chromosome 11 - p Arm

15.5	JW1-51	16	4	0.25	Kidney	CR 51:1071
pter-pl3	D11S17	6	0	0	Liver	CCG 48:72
13	D11S18	11	1	0.09	Liver	CCG 48:72
13	D11S21	5	0	0	Liver	CCG 48:72
15	HBBC	8	1	0.12	Liver	CCG 48:72
15.3-15.4	D11S1243	57	14	0.25	Lung	GCC 13:40
14	D11S1246	57	17	0.3	Lung	GCC 13:40
15.2-15.3	D11S1250	50	17	0.34	Lung	GCC 13:40
15.4-15.5	D11S1251	66	21	0.32	Lung	GCC 13:40
11.2-12	D11S1252	54	13	0.24	Lung	GCC 13:40
15.4-15.5	D11S1254	39	12	0.31	Lung	GCC 13:40
Unknown	HRAS-INS-HBG	1	1	1	Lung	CR 50:2303
Unknown	HRAS-INS-HBG	27	4	0.15	Lung	CR 50:2303
Unknown	HRAS-INS-HBG	1	0	0	Lung	CR 50:2303
Unknown	HRAS-INS-HBG	13	4	0.31	Lung	CR 50:2303
Unknown	HRAS-INS-HBG	3	0	0	Lung	CR 50:2303
15.5	ST5	4	0	0	Lung	PN 91:5513
15.5	ST5	1	0	0	Lung	PN 91:5513
15.5	ST5	9	0	0	Lung	PN 91:5513
Unknown	D11S:922-904	32	4	0.12	Melanoma	CR 56:589
Unknown	Unknown	11	2	0.18	Ovary	IJC 52:575
15	Unknown	5	1	0.2	Ovary	O 5:219
15	Unknown	9	4	0.44	Ovary	O 5:219
Unknown	CALCA-HRAS1-INS-PTH	17	9	0.53	Ovary	GO 55:198
pter-pl3	D11S17	17	6	0.35	Ovary	BRJ 66:103
Unknown	D11S:554-B75-971	18	6	0.33	Ovary	BJC 72:193
Unknown	RAS-CAT-D11S16	34	12	0.35	Ovary	CR 53:2393
15.5	Unknown	3	0	0	Pancreas	CR 54:2761
Unknown	D11S1323	7	2	0.29	Pediatric	HG 97:163
Unknown	D11S1338	14	3	0.21	Pediatric	HG 97:163
Unknown	D11S937	10	1	0.1	Pediatric	HG 97:163
13	WT1	16	8	0.5	Pediatric	HG 97:163
Unknown	Unknown	11	0	0	Prostate	CSurveys 1
Unknown	Unknown	10	0	0	Prostate	PNAS 87:87
Unknown	CALCA-HRAS1-HBG2	15	0	0	Prostate	G 11:530
Unknown	D11S2351	40	16	0.4	Stomach	CR 56:268
Unknown	D11S324	8	3	0.38	Testis	GCC 9:153
Unknown	D11S324	7	3	0.43	Testis	GCC 9:153
Unknown	D11S417	11	3	0.27	Testis	GCC 9:153
Unknown	D11S417	5	3	0.6	Testis	GCC 9:153
Unknown	FSHB	4	0	0	Testis	GCC 9:153
Unknown	FSHB	8	3	0.38	Testis	GCC 9:153
Unknown	FSHB	7	2	0.29	Testis	GCC 7:96
13	WT1	10	5	0.5	Testis	GCC 7:96
Unknown	D11S740	8	1	0.12	Uterus	GCC 9:119
13	WT1	24	0	0	Uterus	CR 54:4294

Chromosome 11 - p Arm

SUM	4917	1151	0.23
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Chromosome 11 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
12-13.2	PYGM	12	5	0.42	Breast	CR 54:4586
12-13.3	PYGM-INT2	36	24	0.67	Breast	CR 55:467
12-13.2	PYGM	30	5	0.17	Cervix	PNAS 91:6953
12-13.2	PYGM	3	2	0.67	Endocrine	GCC 12:73
12-13.2	PYGM	16	6	0.38	Endocrine	CR 56:599
12-13.2	PYGM	4	2	0.5	Endocrine	CR 51:1154
12-13.2	PYGM	42	5	0.12	Esophageal	GCC 10:177
12-13.2	PYGM	15	2	0.13	Kidney	CR 51:5817
12-13.2	PYGM	13	0	0	Prostate	G 11:530
12-13.2	PYGM	7	2	0.29	Stomach	HG 89:445
12	CD20	12	3	0.25	Ovary	BJC 67:268
Unknown	PGA	11	0	0	Colon	CCG 48:167
Unknown	PGA	6	1	0.17	Endocrine	CR 51:1154
Unknown	PGA	15	2	0.13	Testis	GCC 7:96
Unknown	PGA	15	2	0.13	Testis	LI 73:606
13	FGF3	40	4	0.1	Breast	CR 54:6270
13	FGF3	16	3	0.19	Ovary	BJC 67:268
13	D11S913	36	0	0	Esophageal	IJC 69:1
13.1	D11S97	25	7	0.28	Cervix	PNAS 91:6953
13.1	D11S97	23	4	0.17	Testis	GCC 13:249
12-13.2	D11S146	6	2	0.33	Endocrine	CR 51:1154
12-13.2	D11S146	15	1	0.07	Kidney	CR 51:5817
12-13.2	D11S146	23	3	0.13	Liver	CR 51:89
12-13.2	D11S146	10	1	0.1	Ovary	BJC 67:268
13	WT-1	14	7	0.5	Bladder	HG 91:455
13	WT-1	13	4	0.31	Breast	CR 54:6270
13	WT-1	20	6	0.3	Cervix	PNAS 91:6953
13	WT-1	52	5	0.1	Lung	GCC 10:183
13	WT-1	21	4	0.19	Lung	CR 54:5643
13	WT-1	2	1	0.5	Lung	CR 54:5643
13	WT-1	4	0	0	Lung	PN 91:5513
13	WT-1	1	0	0	Lung	PN 91:5513
13	WT-1	6	0	0	Lung	PN 91:5513
13	WT-1	4	1	0.25	Lung	CR 54:5643
13	INT2	22	8	0.36	Bladder	CR 55:5213
13	INT2	3	0	0	Breast	CR 53:3804
13	INT2	12	0	0	Breast	CR 50:7184
13	INT2	34	5	0.15	Breast	CR 53:4356
13	INT2	9	1	0.11	Cervix	GCC 9:119
13	INT2	22	1	0.05	Cervix	CR 54:4481
13	INT2	3	1	0.33	Cervix	CR 54:4481
13	INT2	15	0	0	Cervix	CR 49:3598
13	INT2	22	8	0.36	Cervix	PNAS 91:6953
13	INT2	22	7	0.32	Colon	GCC 6:45
13	INT2	5	2	0.4	Endocrine	GCC 12:73
13	INT2	11	3	0.27	Endocrine	CR 51:1154

Chromosome 11 - q Arm

13	INT2	9	0	0	Esophageal	CR 51:2113
13	INT2	13	6	0.46	Head&Neck	CR 54:1152
13	INT2	9	3	0.33	Kidney	CR 51:820
13	INT2	9	3	0.33	Kidney	CR 51:5817
13	INT2	4	1	0.25	Kidney	CR 51:1071
13	INT2	7	1	0.14	Liver	CR 51:4367
13	INT2	11	3	0.27	Lung	PNAS 86:5099
13	INT2	3	1	0.33	Lung	PNAS 86:5099
13	INT2	11	2	0.18	Lung	PNAS 86:5099
13	INT2	24	3	0.12	Lung	CR 52:2478
13	INT2	6	0	0	Ovary	CR 50:2724
13	INT2	21	0	0	Ovary	IJC 54:546
13	INT2	19	1	0.05	Ovary	CR 51:5118
13	INT2	8	2	0.25	Stomach	HG 89:445
13	INT2	18	0	0	Stomach	CR 51:2926
13	INT2	11	1	0.09	Stomach	CR 48:2988
13	INT2	27	4	0.15	Testis	O 9:2245
13	INT2	4	2	0.5	Testis	O 9:2245
13	INT2	3	1	0.33	Testis	CCG 52:72
13	INT2	4	1	0.25	Testis	CCG 52:72
13	INT2	11	2	0.18	Uterus	GCC 9:119
13	INT2	5	1	0.2	Uterus	CR 51:5632
13.2-22	D11S141	4	0	0	Stomach	HG 89:445
13	D11S534	23	6	0.26	Cervix	BJC 71:814
13	D11S534	13	4	0.31	Ovary	Unknown
Unknown	D11S533	38	12	0.32	Cervix	PNAS 91:6953
Unknown	D11S533	21	5	0.24	Endocrine	GCC 13:9
Unknown	D11S533	16	4	0.25	Ovary	GO 55:245
Unknown	D11S911	23	3	0.13	Cervix	CR 56:197
23.3	D11S901	39	13	0.33	Breast	CR 54:4586
23.3	D11S901	33	11	0.33	Cervix	PNAS 91:6953
23.3	D11S901	21	6	0.29	Stomach	CR 56:268
14-21	TYR	2	0	0	Lung	PN 91:5513
14-21	TYR	7	0	0	Lung	PN 91:5513
14-21	TYR	7	1	0.14	Lung	PN 91:5513
14-21	TYR	16	3	0.19	Ovary	BJC 67:268
14-21	TYR	3	2	0.67	Stomach	HG 89:445
22-23	D11S923	36	2	0.06	Esophageal	IJC 69:1
22	D11S35	28	7	0.25	Breast	CR 54:6270
22	D11S35	34	12	0.35	Breast	CR 54:4586
22	D11S35	21	12	0.57	Cervix	PNAS 91:6953
22	D11S35	34	10	0.29	Stomach	CR 56:268
22	D11S35	33	4	0.12	Uterus	CR 54:4294
22	STMY1	12	6	0.5	Colon	GCC 6:45
22	STMY1	11	6	0.55	Ovary	BJC 67:268
22	STMY1	7	2	0.29	Stomach	HG 89:445

Chromosome 11 - q Arm

22-23	DRD2	68	23	0.34	Colon	BJC 70:395
Unknown	D11S1341	8	3	0.38	Stomach	CR 56:268
22.3-23.3	D11S144	6	1	0.17	Brain	CR 49:6572
22.3-23.3	D11S144	19	13	0.68	Cervix	PNAS 91:6953
22.3-23.3	D11S144	15	3	0.2	Esophageal	CR 54:2996
22.3-23.3	D11S144	17	5	0.29	Ovary	BJC 67:268
22.3-23.3	D11S144	4	2	0.5	Pancreas	CR 54:2761
22.3-23.3	D11S144	21	4	0.19	Sarcoma	CR 52:2419
22.3-23.3	D11S144	4	0	0	Stomach	HG 89:445
23.3	D11S29	47	15	0.32	Breast	CR 54:6270
23.3	D11S29	1	0	0	Breast	CR 53:3804
23.3	D11S29	25	25	1	Cervix	BJC 71:814
23.3	D11S29	2	1	0.5	Colon	GCC 6:45
23.3	D11S29	12	7	0.58	Melanoma	GCC 7:169
23.3	D11S29	15	7	0.47	Ovary	BJC 67:268
23.3	D11S29	10	6	0.6	Stomach	CR 56:268
23	CD3	7	4	0.57	Colon	GCC 6:45
23.3	CD3	1	0	0	Lung	PN 91:5513
23.3	CD3	9	0	0	Lung	PN 91:5513
23.3	CD3	3	0	0	Lung	PN 91:5513
23.3	CD3	16	7	0.44	Ovary	BJC 67:268
23	CD3	4	2	0.5	Stomach	HG 89:445
23.3	CD3	36	8	0.22	Stomach	CR 56:268
23	D11S528	42	16	0.38	Breast	CR 54:6270
23	D11S528	44	7	0.16	Stomach	CR 56:268
22.3-23	THY1	33	14	0.42	Breast	CR 54:4591
22.3-23	THY1	6	1	0.17	Stomach	HG 89:445
23.3-pter	D11S147	12	8	0.67	Ovary	BJC 67:268
22-23.3	APOC3	35	12	0.34	Breast	CR 54:4586
22-23.3	APOC3	30	19	0.63	Cervix	PNAS 91:6953
22-23.3	APOC3	22	0	0	Pediatric	HG 97:163
Unknown	D11S836	17	6	0.35	Ovary	Unknown
Unknown	D11S934	30	5	0.17	Cervix	CR 56:197
23	ETS1	5	3	0.6	Colon	GCC 6:45
23	ETS1	1	0	0	Lung	PN 91:5513
23	ETS1	4	0	0	Lung	PN 91:5513
23	ETS1	5	0	0	Lung	PN 91:5513
23	ETS1	1	0	0	Testis	CCG 52:72
Unknown	D11S910	22	3	0.14	Head&Neck	CR 54:4756
Unknown	D11S910	31	0	0	Head&Neck	CR 54:4756
Unknown	D11S910	6	3	0.5	Kidney	GCC 12:76
Unknown	D11S910	30	5	0.17	Melanoma	CR 56:589
22.3-23	D11S968	33	14	0.42	Breast	CR 54:4586
22.3-23	D11S968	25	14	0.56	Cervix	PNAS 91:6953
22.3-23	D11S968	5	1	0.2	Kidney	PNAS 92:2854
22.3-23	D11S968	17	1	0.06	Kidney	PNAS 92:2854

Chromosome 11 - q Arm

22.3-23	D11S968	17	1	0.06	Kidney	PNAS 92:2854
Unknown	Unknown	16	1	0.06	Brain	CR 50:5784
13	Unknown	25	1	0.04	Breast	JNCI 84:506
Unknown	D11S485	16	9	0.56	Cervix	PNAS 91:6953
13	Unknown	7	0	0	Endocrine	N 328:524
Unknown	D11S129	7	1	0.14	Endocrine	CR 51:1154
Unknown	D11S1383	5	4	0.8	Endocrine	CR 56:599
Unknown	D11S460	7	3	0.43	Endocrine	GCC 12:73
Unknown	D11S476	2	1	0.5	Endocrine	GCC 12:73
Unknown	D11S527	7	5	0.71	Endocrine	CR 56:599
Unknown	D11S546	4	0	0	Endocrine	GCC 12:73
Unknown	D11S614	22	5	0.23	Endocrine	CR 56:599
Unknown	D11S787	6	4	0.67	Endocrine	CR 56:599
Unknown	D11S873	23	6	0.26	Endocrine	CR 56:599
Unknown	D11S874	13	3	0.23	Endocrine	CR 56:599
Unknown	D11S490	19	9	0.47	Head&Neck	CR 54:1152
13	Unknown	7	0	0	Liver	BJC 67:1007
13	Unknown	10	0	0	Liver	BJC 64:1083
13-23	D11S24	2	0	0	Liver	JJ 81:108
14-22.3	D11S1240	53	12	0.23	Lung	GCC 13:40
13.1-13.4	D11S1253	67	13	0.19	Lung	GCC 13:40
21-23.2	D11S1256	67	21	0.31	Lung	GCC 13:40
14-22.3	D11S1260	20	8	0.4	Lung	GCC 13:40
13.4-14	D11S1261	39	11	0.28	Lung	GCC 13:40
23.2-23.3	D11S1263	65	11	0.17	Lung	GCC 13:40
23.2-23.3	D11S1265	50	14	0.28	Lung	GCC 13:40
14-22.3	D11S1268	30	10	0.33	Lung	GCC 13:40
13-23	D11S24	2	0	0	Lung	PN 84:9252
24	D11S488	17	5	0.29	Ovary	GO 55:245
Unknown	D11S85	15	5	0.33	Ovary	CR 53:2393
13	FOLR1	14	1	0.07	Ovary	BJC 67:268
13	Unknown	8	3	0.38	Pancreas	BJC 65:809
Unknown	D11S1818	38	11	0.29	Stomach	CR 56:268
13-23	D11S24	2	0	0	Stomach	CR 48:2988
13-23	D11S24	1	0	0	Uterus	CR 51:5632
Unknown	D11S420	19	0	0	Uterus	CR 54:4294
SUM		2978	764	0.26		

Chromosome 12 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
12.1	KRAS2	3	0	0	Uterus	CR 51:5632
Unknown	D12S16	16	1	0.06	Brain	CR 50:5784
Unknown	D12S16	12	2	0.17	Breast	CR 50:7184
Unknown	D12S16	23	2	0.09	Breast	CR 53:4356
Unknown	D12S2	16	2	0.12	Cervix	CR 54:4481
Unknown	D12S87	24	2	0.08	Cervix	CR 56:197
Unknown	D12S89	25	2	0.08	Cervix	CR 56:197
12.1	KRAS2	7	0	0	Colon	N 331:273
Unknown	D12S77	18	2	0.11	Endocrine	CR 56:599
Unknown	D12S16	26	1	0.04	Esophageal	CR 54:2996
Unknown	D12S16	7	2	0.29	Esophageal	GCC 10:177
Unknown	D12S62	28	5	0.18	Head&Neck	CR 54:1152
Unknown	D12S98	19	1	0.05	Head&Neck	CR 54:4756
Unknown	D12S98	17	0	0	Head&Neck	CR 54:4756
Unknown	D12S16	10	0	0	Kidney	CR 51:820
Unknown	D12S94-D12S77	5	1	0.2	Kidney	PNAS 92:2854
Unknown	D12S94-D12S77	20	0	0	Kidney	PNAS 92:2854
Unknown	D12S98	6	3	0.5	Kidney	GCC 12:76
Unknown	Unknown	43	8	0.19	Leukemia	B 86:3869
Unknown	Unknown	35	8	0.23	Leukemia	B 86:3869
Unknown	D12S58	44	9	0.2	Leukemia	B 86:3869
Unknown	D12S64	54	7	0.13	Leukemia	B 86:3869
Unknown	D12S69	46	4	0.09	Leukemia	B 86:3869
Unknown	D12S89	82	21	0.26	Leukemia	B 87:3368
Unknown	D12S89	50	11	0.22	Leukemia	B 86:3869
Unknown	D12S91	48	9	0.19	Leukemia	B 86:3869
Unknown	D12S94-D12S77	51	6	0.12	Leukemia	B 86:3869
Unknown	D12S:89-91	50	13	0.26	Leukemia	CR 55:5377
Unknown	D12S16	12	1	0.08	Liver	CR 51:89
12.1	KRAS2	4	0	0	Liver	CCG 48:72
Unknown	D12S16	25	5	0.2	Lung	CR 52:2478
12.1	KRAS2	3	1	0.33	Lung	PN 84:9252
Unknown	D12S98	19	0	0	Melanoma	CR 56:589
12.1	KRAS2	2	0	0	Neuroblastom a	CR 49:1095
13.3-12.3	A2M	10	1	0.1	Ovary	IJC 54:546
Unknown	D12S16	8	3	0.38	Ovary	CR 51:5118
12-PTER	PRVWF	16	1	0.06	Ovary	BJC 69:429
12.1	KRAS2	7	0	0	Ovary	CR 50:2724
Unknown	PRB1	23	2	0.09	Ovary	CR 53:2393
Unknown	D12S16	9	1	0.11	Prostate	G 11:530
12.1	KRAS2	4	1	0.25	Stomach	CR 48:2988
12.1	KRAS2	7	0	0	Testis	GCC 13:249
Unknown	PRB1-PRB4	11	2	0.18	Testis	LI 73:606
Unknown	D12S61	14	1	0.07	Uterus	CR 54:4294
12.1	KRAS2	3	0	0	Uterus	CR 51:5632

Chromosome 12 - p Arm

SUM	959	141	0.15
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Chromosome 12 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	IGF1	11	1	0.09	Uterus	CR 54:4294
Unknown	Unknown	14	1	0.07	Brain	CR 50:5784
Unknown	D12S17	19	1	0.05	Breast	CR 50:7184
14-24.1	D12S7	35	2	0.06	Breast	GCC 2:191
Unknown	D12S17	8	1	0.12	Cervix	GCC 9:119
Unknown	D12S7	31	1	0.03	Cervix	CR 54:4481
Unknown	D12S78	31	6	0.19	Cervix	CR 56:197
Unknown	D12S83	22	1	0.05	Cervix	CR 56:197
Unknown	D12S17	19	1	0.05	Colon	CCG 48:167
Unknown	D12S17	17	4	0.24	Colon	IJC 53:382
14-24.1	D12S7	22	3	0.14	Colon	N 331:273
14-qter	D12S8	24	4	0.17	Colon	N 331:273
24.3-qter	D12S11	13	0	0	Endocrine	N 328:524
Unknown	D12S392	16	1	0.06	Endocrine	CR 56:599
Unknown	D12S43	23	0	0	Endocrine	GCC 13:9
Unknown	D12S14	18	3	0.17	Esophageal	CR 54:2996
Unknown	D12S17	9	1	0.11	Esophageal	CR 51:2113
Unknown	D12S17	34	3	0.09	Esophageal	GCC 10:177
Unknown	D12S17	23	2	0.09	Esophageal	CR 54:2996
Unknown	D12S60	24	6	0.25	Head&Neck	CR 54:1152
Unknown	D12S86	24	4	0.17	Head&Neck	CR 54:4756
Unknown	D12S86	18	0	0	Head&Neck	CR 54:4756
Unknown	D12S17	24	0	0	Kidney	CR 51:820
Unknown	D12S86	6	3	0.5	Kidney	GCC 12:76
Unknown	D12S97-D12S86	19	0	0	Kidney	PNAS 92:2854
Unknown	D12S97-D12S86	6	0	0	Kidney	PNAS 92:2854
24.3-qter	Unknown	12	1	0.08	Liver	BJC 64:1083
24.3-qter	Unknown	7	0	0	Liver	BJC 67:1007
Unknown	D12S17	14	1	0.07	Liver	CR 51:89
Unknown	D12S17	15	1	0.07	Liver	JJCR 81:108
Unknown	D12S17	29	4	0.14	Lung	CR 52:2478
Unknown	D12S86	23	0	0	Melanoma	CR 56:589
Unknown	D12S17	25	6	0.24	Ovary	CR 53:2393
Unknown	D12S17	15	5	0.33	Ovary	CR 51:5118
Unknown	D12S60	15	2	0.13	Ovary	BJC 69:429
22-24.2	PAH	26	2	0.08	Ovary	IJC 54:546
24.3-qter	Unknown	13	0	0	Pancreas	BJC 65:809
24.3-qter	Unknown	6	3	0.5	Pancreas	CR 54:2761
Unknown	D12S17	6	0	0	Pancreas	CR 54:2761
14-24.1	D12S7	17	1	0.06	Prostate	G 11:530
Unknown	D12S17	26	5	0.19	Sarcoma	CR 52:2419
CEN-q14	D12S4	5	1	0.2	Sarcoma	CR 52:2419
2.4-ter	Unknown	11	6	0.55	Stomach	BJC 59:750
24.3-qter	D12S11	32	5	0.16	Stomach	HG 92:244
Unknown	D12S17	41	11	0.27	Stomach	CR 51:2926
12-13.2	COL2A1	11	0	0	Testis	GCC 13:249

Chromosome 12 - q Arm

24.3-qter	D12S11	30	0	0	Testis	GCC 13:249
Unknown	D12S12	15	7	0.47	Testis	O 9:2245
Unknown	D12S14	19	3	0.16	Testis	O 9:2245
Unknown	D12S15	14	1	0.07	Testis	O 9:2245
Unknown	D12S17	26	7	0.27	Testis	O 9:2245
CEN-q14	D12S4	23	4	0.17	Testis	O 9:2245
Unknown	D12S6	17	7	0.41	Testis	O 9:2245
14-24.1	D12S7	6	1	0.17	Testis	LI 73:606
14-24.1	D12S7	15	0	0	Testis	GCC 13:249
Unknown	D12S7	1	0	0	Testis	CCG 52:72
Unknown	D12S7	3	0	0	Testis	CCG 52:72
Unknown	D12S7	1	0	0	Testis	CCG 52:72
Unknown	D12S7	19	8	0.42	Testis	O 9:2245
14-qter	D12S8	8	1	0.12	Testis	O 9:2245
Unknown	D12S17	23	4	0.17	Uterus	GCC 9:119
Unknown	D12S60	17	1	0.06	Uterus	CR 54:4294
Unknown	IGF1	11	1	0.09	Uterus	CR 54:4294
SUM		1096	147	0.13		

Chromosome 13 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
12	D13S36	19	5	0.26	Ovary	IJC 54:546
12	D13S36	19	3	0.16	Ovary	IJC 52:575
12.3	D13S11	9	3	0.33	Ovary	IJC 54:546
12.3	D13S11	6	5	0.83	Sarcoma	CGC 53:45
Unknown	D13S115	13	6	0.46	Head&Neck	CR 54:1152
Unknown	D13S115	16	2	0.12	Ovary	BJC 69:429
Unknown	D13S221	28	7	0.25	Bladder	Unknown
Unknown	D13S221	39	17	0.44	Breast	GCC 13:291
12.3	D13S6	4	2	0.5	Breast	PNAS 84:2372
12.3	D13S6	13	5	0.38	Colon	IJC 53:382
12.3	D13S6	1	0	0	Colon	CCG 48:167
12.3	D13S6	8	2	0.25	Ovary	IJC 54:546
12.3	D13S6	9	0	0	Stomach	G 2:180
12.3	D13S6	7	2	0.29	Uterus	CR 51:5632
Unknown	D13S289	35	17	0.49	Breast	GCC 13:291
12	FLT1	7	0	0	Brain	CR 54:1397
12	FLT1	9	3	0.33	Brain	CR 54:1397
12	FLT1	18	6	0.33	Ovary	CR 54:605
12	FLT1	5	1	0.2	Ovary	BJC 69:429
12.3	D13S33	21	4	0.19	Ovary	IJC 54:546
12.3	D13S33	23	6	0.26	Ovary	IJC 52:575
12	D13S260	43	13	0.3	Breast	GCC 13:291
13	D13S1	94	26	0.28	Bladder	O 6:2305
14-12	D13S1	34	7	0.21	Breast	GE 5:554
13	D13S1	8	3	0.38	Breast	PNAS 84:2372
13	D13S1	13	4	0.31	Breast	GCC 2:191
13	D13S1	7	2	0.29	Cervix	CR 49:3598
14-12	D13S1	11	1	0.09	Colon	JNCI 84:1100
13	D13S1	15	7	0.47	Colon	IJC 53:382
12	D13S1	12	1	0.08	Colon	CCG 48:167
13	D13S1	14	4	0.29	Esophageal	CR 54:2996
13	D13S1	10	2	0.2	Kidney	CR 51:1071
13	D13S1	25	5	0.2	Liver	JJCR 84:893
14-12	D13S1	15	5	0.33	Liver	CR 54:281
14-12	D13S1	5	2	0.4	Liver	CCG 48:12
12	D13S1	9	0	0	Liver	JJCR 81:108
14-12	D13S1	9	6	0.67	Liver	CR 51:4367
13	D13S1	19	8	0.42	Lung	PN 84:9252
14-12	D13S1	8	7	0.88	Lung	CR 49:5130
12	D13S1	1	0	0	Lung	PN 84:9252
13	D13S1	5	0	0	Neuroblastom	CR 49:1095
13	D13S1	15	2	0.13	Ovary	IJC 54:546
13	D13S1	12	9	0.75	Sarcoma	CR 52:2419
13	D13S1	6	0	0	Stomach	HG 89:445
14-12	D13S1	10	1	0.1	Stomach	CR 48:2988

Chromosome 13 - q Arm

14-12	D13S1	11	1	0.09	Testis	LI 73:606
13	D13S1	3	0	0	Testis	CCG 52:72
13	D13S1	3	1	0.33	Testis	CCG 52:72
13	D13S1	1	0	0	Testis	CCG 52:72
13	D13S1	8	1	0.12	Uterus	CR 51:5632
12	D13S267	32	16	0.5	Breast	GCC 13:291
14	D13S218	140	33	0.24	Leukemia	CR 55:2044
12	D13S263	45	20	0.44	Breast	GCC 13:291
14	D13S22	17	5	0.29	Breast	GE 5:554
14	D13S22	11	3	0.27	Breast	GE 5:554
14	D13S22	12	0	0	Pediatric	CR 50:3279
14	D13S22	8	7	0.88	Sarcoma	GCC 53:44
14	D13S153	42	15	0.36	Breast	GCC 13:291
14.3	D13S133	18	10	0.56	Head&Neck	CR 54:152
14.3	D13S133	6	3	0.5	Kidney	GCC 12:76
14.3	D13S133	140	5	0.04	Leukemia	CR 55:2044
14.3	D13S133	11	0	0	Ovary	CR 54:605
14.3	D13S133	18	11	0.61	Ovary	CR 54:605
14.3	D13S133	21	7	0.33	Prostate	HUPATH 27:28
14.3-21.1	D13S31	29	9	0.31	Ovary	IJC 52:575
14.3-21	D13S31	26	6	0.23	Ovary	IJC 54:546
14	RB	94	28	0.3	Bladder	O 6:2305
14	RB	9	4	0.44	Brain	O 6:445
14	RB	20	3	0.15	Breast	AJP 140:215
14	RB	38	6	0.16	Breast	CR 53:4356
14.1	RB	14	5	0.36	Breast	JNCI 84:506
14	RB	10	4	0.4	Breast	GCC 4:113
14	RB	32	12	0.38	Breast	GE 5:554
14	RB	37	12	0.32	Breast	GCC 4:113
14	RB	90	23	0.26	Breast	CR 52:2991
14	RB	14	0	0	Cervix	BJC 67:71
14	RB	27	9	0.33	Colon	CR 52:741
14	RB	25	12	0.48	Colon	IJC 53:382
14.1	RB	156	18	0.12	Colon	BJC 64:475
14	RB	39	10	0.26	Colon	GAST 104:163
14	RB	8	0	0	Colon	JNCI 84:1100
14	RB	6	0	0	Colon	JNCI 84:1100
14	RB	42	0	0	Endocrine	C 74:693
14	RB	29	17	0.59	Esophageal	C 73:2472
14	RB	40	19	0.47	Esophageal	CR 51:5766
14	RB	8	1	0.12	Esophageal	CR 51:2113
14	RB	16	5	0.31	Esophageal	CR 54:2996
14	RB	50	24	0.48	Esophageal	CR 52:6525
14	RB	29	17	0.59	Head&Neck	C 73:2472
14	RB	11	4	0.36	Liver	CR 54:281
14	RB	11	3	0.27	Liver	CR 51:4367

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14	RB	9	1	0.11	Liver	CR 51:4367
14	RB	67	13	0.19	Lung	O 8:1913
14	RB	16	0	0	Lung	O 9:39
14	RB	7	2	0.29	Lung	CR 54:5643
14	RB	20	12	0.6	Lung	O 8:1913
14	RB	8	0	0	Lung	S 241:353
14	RB	3	2	0.67	Lung	CL 71:67
14	RB	8	6	0.75	Lung	O 9:39
14	RB	76	28	0.37	Lung	O 8:1913
14	RB	27	14	0.52	Lung	CR 54:5643
14	RB	59	22	0.37	Lung	O 10:937
14	RB	5	4	0.8	Lung	CR 54:5643
14	RB	2	1	0.5	Lung	CL 71:67
14	RB	7	1	0.14	Ovary	GO 55:245
14	RB	13	8	0.62	Ovary	IJC 58:663
14	RB	31	23	0.74	Ovary	CR 54:610
14	RB	39	13	0.33	Ovary	IJC 54:546
14.1	RB	17	2	0.12	Ovary	CR 54:610
14	RB	33	9	0.27	Ovary	IJC 52:575
14	RB	48	25	0.52	Ovary	CR 54:610
14	RB	9	0	0	Pediatric	CR 50:3279
14	RB	13	3	0.23	Prostate	PNAS 87:8751
14.1	RB	9	6	0.67	Prostate	BJU 73:390
14	RB	19	7	0.37	Prostate	HUPATH 27:28
14	RB	40	24	0.6	Prostate	BJC 70:1252
14	RB	7	5	0.71	Sarcoma	CR 52:2419
14	RB	13	4	0.31	Stomach	LI 74:835
14	RB	31	12	0.39	Testis	O 9:2245
Unknown	D13S155	6	3	0.5	Kidney	GCC 12:76
Unknown	D13S155	32	3	0.09	Melanoma	CR 56:589
14.1	D13S118	21	7	0.33	Prostate	HUPATH 27:28
21.1-21.2	D13S26	27	17	0.63	Ovary	GO 47:137
21-qter	D13S12	7	1	0.14	Liver	PNAS 86:8852
21-qter	D13S12	4	4	1	Sarcoma	CCG 53:45
22	D13S2	94	26	0.28	Bladder	O 6:2305
Unknown	D13S2	6	1	0.17	Breast	GCC 2:191
22	D13S2	7	3	0.43	Breast	PNAS 84:2372
22	D13S2	2	0	0	Cervix	CR 49:3598
22	D13S2	4	1	0.25	Cervix	CR 54:4481
22	D13S2	10	3	0.3	Colon	IJC 53:382
22	D13S2	8	0	0	Colon	CCG 48:167
22	D13S2	4	1	0.25	Colon	CCG 48:167
22	D13S2	17	7	0.41	Esophageal	CR 54:2996
22	D13S2	6	2	0.33	Kidney	CR 51:1071
22	D13S2	6	4	0.67	Liver	CCG 48:72
22	D13S2	13	3	0.23	Liver	CR 51:89

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Unknown	D13S2	13	0	0	Liver	JJCR 81:108
22	D13S2	21	12	0.57	Lung	PN 84:9252
22	D13S2	12	2	0.17	Lung	JJCR 80:924
Unknown	D13S2	9	7	0.78	Lung	CR 49:5130
22	D13S2	7	1	0.14	Neuroblastom a	CR 49:1095
Unknown	D13S2	10	3	0.3	Ovary	IJC 54:546
22	D13S2	8	6	0.75	Sarcoma	CR 52:2419
22	D13S2	10	3	0.3	Stomach	CR 52:3099
22	D13S2	9	1	0.11	Stomach	HG 92:244
22	D13S2	11	2	0.18	Stomach	CR 48:2988
22	D13S2	6	4	0.67	Stomach	G 2:180
Unknown	D13S2	7	1	0.14	Stomach	HG 89:445
Unknown	D13S2	14	4	0.29	Testis	O 9:2245
22	D13S2	4	1	0.25	Uterus	CR 51:5632
22-31	D13S170	47	11	0.23	Breast	GCC 13:291
22-31	D13S170	29	11	0.38	Head&Neck	CR 54:4756
22-31	D13S170	20	0	0	Head&Neck	CR 54:4756
31	D13S4	1	1	1	Breast	GCC 2:191
Unknown	D13S4	26	3	0.12	Breast	GE 5:554
Unknown	D13S4	5	2	0.4	Breast	PNAS 84:2372
Unknown	D13S4	10	0	0	Cervix	CR 49:3598
31	D13S4	8	0	0	Colon	JNCI 84:1100
Unknown	D13S4	1	0	0	Colon	CCG 48:167
Unknown	D13S4	19	12	0.63	Colon	IJC 53:382
Unknown	D13S4	12	4	0.33	Esophageal	CR 54:2996
Unknown	D13S4	4	0	0	Liver	JJCR 81:108
31	D13S4	19	10	0.53	Lung	PN 84:9252
31	D13S4	16	3	0.19	Lung	JJCR 80:924
Unknown	D13S4	5	5	1	Lung	CR 49:5130
31	D13S4	8	0	0	Neuroblastom a	CR 49:1095
Unknown	D13S4	15	11	0.73	Sarcoma	CR 52:2419
31	D13S4	14	3	0.21	Stomach	HG 92:244
Unknown	D13S4	11	2	0.18	Stomach	G 2:180
Unknown	D13S4	17	2	0.12	Stomach	CR 48:2988
Unknown	D13S4	12	0	0	Uterus	CR 51:5632
22-34	D13S5	26	6	0.23	Breast	GE 5:554
21.3-32	D13S5	4	1	0.25	Breast	PNAS 84:2372
21.3-32	D13S5	15	4	0.27	Colon	IJC 53:382
21.3-32	D13S5	4	0	0	Colon	CCG 48:167
22-34	D13S5	1	0	0	Colon	JNCI 84:1100
22-34	D13S5	22	9	0.41	Ovary	IJC 54:546
21.3-32	D13S5	10	4	0.4	Stomach	G 2:180
22-34	D13S5	7	1	0.14	Stomach	G 2:180
21.3-32	D13S5	5	0	0	Uterus	CR 51:5632
22-34	D13S5	3	0	0	Uterus	CR 51:5632

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21	D13S71	15	2	0.13	Brain	CR 54:1397
21	D13S71	7	0	0	Brain	CR 54:1397
32-34	D13S128	34	12	0.35	Ovary	CR 54:605
34	D13S34	12	5	0.42	Ovary	IJC 52:575
34	D13S34	15	7	0.47	Ovary	IJC 54:546
34	D13S32	28	11	0.39	Ovary	IJC 54:546
34	D13S32	26	12	0.46	Ovary	IJC 52:575
22-31	D13S173	39	7	0.18	Breast	GCC 13:291
34	D13S3	94	26	0.28	Bladder	O 6:2305
Unknown	D13S3	20	3	0.15	Breast	GCC 2:191
34	D13S3	26	4	0.15	Breast	GE 5:554
34	D13S3	7	2	0.29	Breast	PNAS 84:2372
33-34	D13S3	27	3	0.11	Cervix	CR 54:4401
34	D13S3	18	4	0.22	Cervix	CR 49:3598
34	D13S3	15	6	0.4	Colon	IJC 53:382
Unknown	D13S3	6	0	0	Colon	JNCI 84:1100
Unknown	D13S3	4	0	0	Liver	JOCR 81:108
33-34	D13S3	2	1	0.5	Liver	CCG 48:72
34	D13S3	8	4	0.5	Liver	CR 51:4367
34	D13S3	9	4	0.44	Lung	PNAS 86:5099
Unknown	D13S3	23	7	0.3	Lung	PN 84:9252
34	D13S3	11	10	0.91	Lung	CR 49:5130
34	D13S3	24	9	0.38	Lung	PN 84:9252
34	D13S3	9	4	0.44	Lung	PNAS 86:5099
34	D13S3	7	1	0.14	Neuroblastom	CR 49:1095
34	D13S3	21	3	0.14	Ovary	IJC 52:575
34	D13S3	19	4	0.21	Ovary	IJC 54:546
Unknown	D13S3	9	4	0.44	Sarcoma	CR 52:2419
34	D13S3	5	0	0	Stomach	HG 89:445
34	D13S3	20	5	0.25	Stomach	G 2:180
33-34	D13S3	9	1	0.11	Stomach	HG 92:244
Unknown	D13S3	19	5	0.26	Stomach	G 2:180
33-34	D13S3	17	2	0.12	Stomach	CR 48:2988
Unknown	D13S3	1	0	0	Testis	CCG 52:72
34	D13S3	20	8	0.4	Testis	O 9:2245
Unknown	D13S3	4	0	0	Testis	CCG 52:72
Unknown	D13S3	2	0	0	Testis	CCG 52:72
34	D13S3	7	1	0.14	Uterus	CR 51:5632
34	D13S35	17	2	0.12	Ovary	IJC 54:546
34	D13S35	18	2	0.11	Ovary	IJC 52:575
Unknown	D13S52	33	7	0.21	Breast	CR 50:7184
Unknown	D13S52	132	34	0.26	Breast	CR 51:5794
Unknown	D13S52	53	23	0.43	Esophageal	GCC 10:177
Unknown	D13S52	16	3	0.19	Esophageal	CR 51:2113
Unknown	D13S52	22	10	0.45	Esophageal	CR 54:2996
Unknown	D13S52	20	3	0.15	Kidney	CR 51:820

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Unknown	D13S52	26	4	0.15	Liver	CR 51:89
Unknown	D13S52	2	1	0.5	Lung	CR 52:2478
Unknown	D13S52	9	5	0.56	Lung	CR 52:2478
Unknown	D13S52	26	5	0.19	Lung	CR 52:2478
Unknown	D13S52	1	1	1	Lung	CR 52:2478
Unknown	D13S52	27	6	0.22	Ovary	CR 51:5118
34	F7	11	2	0.18	Ovary	IJC 54:546
34	F7	11	2	0.18	Ovary	IJC 54:546
Unknown	BRAC2 (D13S:263-219-220-267-171-260-217)	1	1	1	Bladder	CR 55:4830
Unknown	D13S30	3	0	0	Bladder	CR 51:5405
Unknown	D13S:133-170	30	15	0.5	Bladder	CR 55:5213
Unknown	Unknown	7	1	0.14	Brain	CR 49:6572
Unknown	Unknown	14	2	0.14	Brain	CR 50:5784
32	D13S193	13	2	0.15	Brain	CR 54:1397
32	D13S193	13	0	0	Brain	CR 54:1397
Unknown	RB1-D13S4-D13S63	7	0	0	Brain	CGC 73:122
Unknown	RB1-D13S4-D13S63	18	2	0.11	Brain	CGC 73:122
Unknown	RB1-D13S4-D13S63	10	0	0	Brain	CGC 73:122
Unknown	BRAC2 (D13S:263-219-220-267-171-260-217)	1	1	1	Breast	CR 55:4830
Unknown	BRAC2 (D13S:263-219-220-267-171-260-217)	33	28	0.85	Breast	CR 55:4830
Unknown	D13S7	2	1	0.5	Breast	PNAS 84:2372
Unknown	BRAC2 (D13S:263-219-220-267-171-260-217)	1	1	1	Cervix	CR 55:4830
Unknown		6	0	0	Colon	JNCI 84:1100
Unknown	BRAC2 (D13S:263-219-220-267-171-260-217)	1	1	1	Colon	CR 55:4830
Unknown	D13S10	5	0	0	Colon	CCG 48:167
Unknown	D13S37	21	1	0.05	Colon	CCG 48:167
Unknown	ESD	19	0	0	Colon	CCG 48:167
Unknown	D13S168	18	2	0.11	Endocrine	CR 56:599
Unknown	D13S174-D13S173	20	1	0.05	Kidney	PNAS 92:2854
Unknown	D13S174-D13S173	5	0	0	Kidney	PNAS 92:2854
Unknown	D13S:156-158-164-217-221	24	3	0.12	Leukemia	CR 55:5377
Unknown	Unknown	11	0	0	Liver	BJC 64:1083
Unknown	Unknown	5	0	0	Liver	BJC 67:1007
Unknown	14.2	7	0	0	Liver	BJC 67:1007
p11-q11	D13S11	1	1	1	Liver	PNAS 86:8852
Unknown	Unknown	24	18	0.75	Lung	CR 54:2322
33-qter	Unknown	3	1	0.33	Lung	PN 86:5099
33-qter	Unknown	9	4	0.44	Lung	PN 86:5099

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33-qter	Unknown	9	4	0.44	Lung	PN 86:5099
Unknown	BRAC2 (D13S:263-219-220-267-171-260-217)	6	5	0.83	Ovary	CR 55:4830
Unknown	D13S3-2-1-RB1	32	18	0.56	Ovary	CR 53:2393
Unknown	Unknown	7	0	0	Pancreas	BJC 65:809
Unknown	14.2	10	0	0	Pancreas	BJC 65:809
Unknown	Unknown	13	3	0.23	Prostate	CSurveys 11:
Unknown	BRAC2 (D13S:263-219-220-267-171-260-217)	7	6	0.86	Prostate	CR 55:4830
Unknown	D13S3-D13S5	11	1	0.09	Prostate	G 11:530
Unknown	D13S103	32	5	0.16	Stomach	RG 92:244
Unknown	D13S409	14	2	0.14	Stomach	CR 55:1933
Unknown	Unknown	15	3	0.2	Testis	G 5:134
Unknown	D13S103	9	1	0.11	Testis	GCC 13:249
Unknown	D13S70	13	3	0.23	Testis	GCC 13:249
Unknown	D13S120	15	0	0	Uterus	CR 54:4294
Unknown	D13S122	18	2	0.11	Uterus	CR 54:4294
SUM		5208	1509	0.29		

Band	Marker	Total	Cases wi/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D14S22	24	2	0.08	Esophageal	CR 54:2996
SUM		24	2	0.08		

Chromosome 14 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	TCRD	31	6	0.19	Uterus	CR 54:4294
Unknown	D14S:267-268-51	30	21	0.7	Bladder	CR 55:5213
Unknown	Unknown	19	3	0.16	Brain	CR 50:5784
32	D14S13	14	1	0.07	Brain	CR 49:6572
32.1-32.2	D14S13	26	1	0.04	Brain	CR 55:4696
32.1-32.2	D14S13	26	1	0.04	Brain	CR 55:4696
32	D14S16	26	1	0.04	Brain	CR 55:4696
32	D14S16	26	1	0.04	Brain	CR 55:4696
32.32-33	D14S23	26	0	0	Brain	CR 55:4696
32.32-33	D14S23	26	0	0	Brain	CR 55:4696
24.3	D14S43	26	5	0.19	Brain	CR 55:4696
24.3	D14S43	26	5	0.19	Brain	CR 55:4696
32.1-32.2	D14S45	26	1	0.04	Brain	CR 55:4696
32.1-32.2	D14S45	26	1	0.04	Brain	CR 55:4696
24.3-31	D14S48	26	8	0.31	Brain	CR 55:4696
24.3-31	D14S48	26	8	0.31	Brain	CR 55:4696
32.1-32.2	D14S51	26	3	0.12	Brain	CR 55:4696
32.1-32.2	D14S51	26	3	0.12	Brain	CR 55:4696
12.0-13.0	D14S54	26	2	0.08	Brain	CR 55:4696
12.0-13.0	D14S54	26	2	0.08	Brain	CR 55:4696
23-31	D14S59	26	10	0.38	Brain	CR 55:4696
23-31	D14S59	26	10	0.38	Brain	CR 55:4696
12.0-13.0	D14S70	26	8	0.31	Brain	CR 55:4696
12.0-13.0	D14S70	26	8	0.31	Brain	CR 55:4696
24.3-31	D14S76	26	6	0.23	Brain	CR 55:4696
24.3-31	D14S76	26	6	0.23	Brain	CR 55:4696
12	D14S80	26	7	0.27	Brain	CR 55:4696
12	D14S80	26	7	0.27	Brain	CR 55:4696
31	D14S81	26	7	0.27	Brain	CR 55:4696
31	D14S81	26	7	0.27	Brain	CR 55:4696
32.3	IGH	26	9	0.35	Brain	CR 55:4696
32.3	IGH	26	9	0.35	Brain	CR 55:4696
32	D14S13	60	7	0.12	Breast	CR 53:4356
32	D14S13	29	7	0.24	Breast	GCC 2:191
32	D14S13	47	6	0.13	Breast	CR 50:7184
32	D14S16	17	2	0.12	Breast	GCC 2:191
32.3	IGH	6	2	0.33	Breast	CR 53:3804
32.32-33	D14S1	10	2	0.2	Cervix	CR 49:3598
32.33	D14S20	10	1	0.1	Cervix	CR 54:4481
Unknown	D14S3	7	0	0	Cervix	GCC 9:119
32.1	ARCT	26	6	0.23	Colon	O 8:671
32.32-33	AKT1	10	4	0.4	Colon	O 8:671
32.32-33	D14S1	42	14	0.33	Colon	O 8:671
32.33	D14S1	28	12	0.43	Colon	IJC 53:382
32	D14S13	35	14	0.4	Colon	IJC 53:382
Unknown	D14S16	17	2	0.12	Colon	CCG 48:167

Chromosome 14 - q Arm

32	D14S16	14	7	0.5	Colon	IJC 53:382
32	D14S16	37	18	0.49	Colon	O 8:671
32.32-.33	D14S17	12	5	0.42	Colon	IJC 53:382
32.32-.33	D14S17	20	7	0.35	Colon	O 8:671
32.1-32.32	D14S18	1	1	1	Colon	IJC 53:382
32.32-32.33	D14S19	39	22	0.56	Colon	O 8:671
32.33	D14S19	14	4	0.29	Colon	IJC 53:382
32.33	D14S20	20	10	0.5	Colon	O 8:671
32.1-32.32	D14S21	2	2	1	Colon	IJC 53:382
32.1-32.32	D14S21	23	6	0.26	Colon	O 8:671
32.32-.33	D14S23	23	9	0.39	Colon	IJC 53:382
32.32-.33	D14S23	42	21	0.5	Colon	O 8:671
32.3	IGH	47	26	0.55	Colon	O 8:671
32.1	PI	6	0	0	Colon	O 8:671
Unknown	D14S174	21	0	0	Endocrine	GCC 13:9
32.1-32.2	D14S45	23	0	0	Endocrine	CR 56:599
32	D14S13	23	4	0.17	Esophageal	CR 51:2113
32	D14S13	64	9	0.14	Esophageal	GCC 10:177
32	D14S13	26	4	0.15	Esophageal	CR 54:2996
Unknown	D14S51	23	9	0.39	Head&Neck	CR 54:1152
Unknown	D14S73	20	1	0.05	Head&Neck	CR 54:4756
Unknown	D14S73	18	1	0.06	Head&Neck	CR 54:4756
32	D14S13	36	3	0.08	Kidney	CR 51:820
Unknown	D14S65-D14S81	6	1	0.17	Kidney	PNAS 92:28
Unknown	D14S65-D14S81	22	5	0.23	Kidney	PNAS 92:28
Unknown	Unknown	10	0	0	Liver	BJC 64:108
Unknown	Unknown	5	0	0	Liver	BJC 67:100
32.32-.33	D14S1	3	0	0	Liver	CCG 48:72
32.32-.33	D14S1	17	6	0.35	Liver	JJCR 81:10
32	D14S13	46	5	0.11	Liver	CR 51:89
Unknown	D14S15	2	0	0	Liver	PNAS 86:88
32.32-.33	D14S1	1	1	1	Lung	CR 54:5643
32.32-.33	D14S1	17	7	0.41	Lung	CR 54:5643
32.32-.33	D14S1	8	1	0.12	Lung	CR 54:5643
32.32-.33	D14S1	23	2	0.09	Lung	PN 84:9252
32	D14S13	50	6	0.12	Lung	CR 52:2478
32.33	D14S1	22	7	0.32	Neuroblastom	O 7:1185
32.32-.33	D14S1	16	8	0.5	Neuroblastom	CR 49:1095
32.32-.33	D14S1	19	4	0.21	Neuroblastom	O 7:1185
32.1-32.2	D14S13	24	5	0.21	Neuroblastom	O 7:1185
32	D14S16	13	8	0.62	Neuroblastom	O 7:1185
32.32-.33	D14S17	18	1	0.06	Neuroblastom	O 7:1185

Chromosome 14 - q Arm

32.32-32.33	D14S19	20	4	0.2	Neuroblastom	O 7:1185
32.1-32.32	D14S21	18	1	0.06	Neuroblastom	O 7:1185
11.2-13	MYH6	17	0	0	Neuroblastom	O 7:1185
32.32-.33	D14S1	26	2	0.08	Ovary	IJC 54:546
32	D14S13	28	5	0.18	Ovary	CR 51:5118
32	D14S16	15	7	0.47	Ovary	CR 53:2393
32.33	D14S20	9	3	0.33	Ovary	O 7:1059
Unknown	D14S34	13	7	0.54	Ovary	BJC 69:429
24.3-31	D14S48	9	3	0.33	Ovary	BJC 69:429
Unknown	D14S49	20	5	0.25	Ovary	BJC 69:429
Unknown	D14S50	10	3	0.3	Ovary	BJC 69:429
Unknown	D14S51	17	4	0.24	Ovary	BJC 69:429
Unknown	Unknown	6	0	0	Pancreas	BJC 65:809
32	D14S13	4	0	0	Pancreas	CR 54:2761
32.32-.33	D14S1	7	0	0	Prostate	G 11:530
32	D14S13	29	1	0.03	Sarcoma	CR 52:2419
32.32-.33	D14S1	16	1	0.06	Sarcoma	CR 52:2419
Unknown	D14S44	32	5	0.16	Stomach	CR 48:2986
32.33	D14S20	8	1	0.12	Stomach	HG 92:244
Unknown	D14S44	21	2	0.1	Testis	O 9:2245
32.32-.33	D14S1	10	0	0	Testis	GCC 13:249
Unknown	D14S3	12	1	0.08	Uterus	CR 51:5632
24.3-31	D14S76	28	3	0.11	Uterus	GCC 9:119
11.2-13	MYH6	18	2	0.11	Uterus	CR 54:4294
Unknown	TCRD	31	6	0.19	Uterus	CR 54:4294
SUM		2442	542	0.22		

Chromosome 15 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D15S25	26	4	0.15	Esophageal	CR 54:2996
Unknown	D15S25	9	0	0	Colon	CCG 48:167
Unknown	D15S25	26	4	0.15	Esophageal	CR 54:2996
SUM		35	4	0.11		

Chromosome 15 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
26.1	FES	36	5	0.14	Uterus	CR 54:4294
Unknown	Unknown	18	3	0.17	Brain	CR 50:5784
Unknown	D15S27	7	1	0.14	Brain	CR 49:6572
14-21	D15S1	28	1	0.04	Breast	GCC 2:191
11-12.0	D15S11	34	3	0.09	Breast	CR 53:4356
pter-q13	D15S24	2	1	0.5	Breast	CR 53:3804
Unknown	D15S28	12	2	0.17	Breast	CR 50:7184
Unknown	D15S29	16	4	0.25	Breast	GCC 2:191
14-21	D15S1	6	0	0	Cervix	CR 49:3598
pter-q13	D15S24	23	0	0	Cervix	CR 54:4481
14-21	D15S1	6	1	0.17	Colon	N 331:273
Unknown	ACTC	36	6	0.17	Endocrine	CR 56:599
Unknown	CYP19	33	5	0.15	Endocrine	CR 56:599
14-21	D15S1	5	4	0.8	Endocrine	CR 56:599
Unknown	D15S100	31	5	0.16	Endocrine	CR 56:599
Unknown	D15S107	8	6	0.75	Endocrine	CR 56:599
Unknown	D15S109	8	3	0.38	Endocrine	CR 56:599
Unknown	D15S114	4	4	1	Endocrine	CR 56:599
Unknown	D15S116	21	7	0.33	Endocrine	CR 56:599
Unknown	D15S118	16	5	0.31	Endocrine	CR 56:599
Unknown	D15S125	24	5	0.21	Endocrine	CR 56:599
Unknown	D15S127	10	7	0.7	Endocrine	CR 56:599
Unknown	D15S144	9	7	0.78	Endocrine	CR 56:599
Unknown	D15S165	32	7	0.22	Endocrine	CR 56:599
Unknown	D15S87	20	7	0.35	Endocrine	CR 56:599
Unknown	D15S97	32	8	0.25	Endocrine	CR 56:599
Unknown	GABRB3	31	7	0.23	Endocrine	CR 56:599
Unknown	D15S27	17	2	0.12	Esophageal	GCC 10:177
Unknown	D15S27	27	2	0.07	Esophageal	CR 54:2996
Unknown	D15S117	21	1	0.05	Head&Neck	CR 54:1152
Unknown	D15S118	17	1	0.06	Head&Neck	CR 54:4756
Unknown	D15S118	15	0	0	Head&Neck	CR 54:4756
Unknown	D15S118	6	3	0.5	Kidney	GCC 12:76
Unknown	D15S120-D15S127	21	1	0.05	Kidney	PNAS 92:2854
Unknown	D15S120-D15S127	6	0	0	Kidney	PNAS 92:2854
Unknown	D15S28	18	2	0.11	Kidney	CR 51:820
14-21	D15S1	10	1	0.1	Liver	JJCR 81:108
pter-q13	D15S24	26	3	0.12	Liver	CR 51:89
14-21	D15S1	4	0	0	Lung	NEJ 317:1109
14-21	D15S1	8	0	0	Lung	PN 84:9252
14-21	D15S1	5	2	0.4	Lung	NEJ 317:1109
14-21	D15S1	2	0	0	Lung	NEJ 317:1109
Unknown	D15S28	18	2	0.11	Lung	CR 52:2478
Unknown	D15S118	24	4	0.17	Melanoma	CR 56:589
14-21	D15S1	7	0	0	Neuroblastom	CR 49:1095

Chromosome 15 - q Arm

11-12.0	D15S11	13	1	0.08	Ovary	IJC 54:546
Unknown	D15S2	11	4	0.36	Ovary	CR 53:2393
pter-q13	D15S24	31	2	0.06	Ovary	IJC 54:546
Unknown	D15S28	9	1	0.11	Ovary	CR 51:5118
26.1	FES	15	6	0.4	Ovary	BJC 69:429
pter-q13	D15S24	1	0	0	Pancreas	CR 54:2761
Unknown	D15S29-D15S1	9	0	0	Prostate	G 11:530
14-21	D15S1	9	4	0.44	Sarcoma	CR 52:2419
Unknown	D15S27	12	5	0.42	Sarcoma	CR 52:2419
14-21	D15S1	13	0	0	Stomach	CR 48:2988
Unknown	D15S86	32	5	0.16	Stomach	HG 92:244
pter-q13	D15S24	46	4	0.09	Testis	Q 9:2245
Unknown	D15S86	21	2	0.1	Testis	GCC 13:249
Unknown	CYP19	27	0	0	Uterus	CR 54:4294
14-21	D15S1	6	1	0.17	Uterus	CR 51:5632
26.1	FES	36	5	0.14	Uterus	CR 54:4294
SUM		1015	173	0.17		

Chromosome 16 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Refs
13.3	HBZP1	6	0	0	Prostate	G1
13.3	D16S85	7	0	0	Breast	CR
13.3	D16S85	62	5	0.08	Breast	GCC
13.3	D16S85	8	0	0	Liver	BJC
13.3	D16S85	11	0	0	Liver	BJC
13.3	D16S85	24	5	0.21	Ovary	CR
13.3	D16S85	11	1	0.09	Pancreas	BJC
13.3	D16S85	11	1	0.09	Stomach	HG
13.3	D16S85	22	3	0.14	Testis	GCC
13.3	D16S83	27	8	0.3	Breast	GCC
13.3	D16S83	31	6	0.19	Breast	CR
13.3	D16S83	16	2	0.12	Esophageal	CR
13.3	D16S83	10	0	0	Esophageal	CR
13.3	D16S83	19	5	0.26	Liver	CR
13.3	D16S83	16	1	0.06	Liver	CR
13.3	D16S83	15	6	0.4	Sarcoma	CR
13	D16S84	21	1	0.05	Breast	CR
13	D16S84	43	0	0	Breast	CR
pter-p13.3	D16S84	5	0	0	Cervix	GCC
pter-p13.3	D16S84	28	4	0.14	Esophageal	GCC
pter-p13.3	D16S84	14	1	0.07	Kidney	CR
pter-p13.3	D16S84	22	5	0.23	Lung	CR
pter-p13.3	D16S84	21	7	0.33	Ovary	CR
pter-p13.3	D16S84	9	2	0.22	Uterus	GCC
13.3	HBAI	22	5	0.23	Breast	CR
13.3	HBAI	47	1	0.02	Breast	CR
13.3	HBAI	22	5	0.23	Breast	CR
13.3	HBAI	11	9	0.82	Liver	CR
13.3	HBAI	36	16	0.44	Liver	PNA
Unknown	D16S414	10	0	0	Head&Neck	CR
Unknown	D16S414	19	3	0.16	Head&Neck	CR
Unknown	D16S414	6	3	0.5	Kidney	GCC
Unknown	D16S414	26	1	0.04	Melanoma	CR
13	D16S292	12	0	0	Ovary	BJC
pter-p13	D16S32	21	3	0.14	Breast	CR
pter-p13	D16S32	26	8	0.31	Liver	PNA
pter-p13	D16S32	16	4	0.25	Liver	JJC
pter-p13	D16S32	8	7	0.88	Liver	CR
13.1	MRP	13	5	0.38	Leukemia	LAN
13.11	D16S131	8	1	0.12	Breast	CR
13.11	D16S131	13	6	0.46	Liver	PNA
12.2	D16S159	34	6	0.18	Breast	CR
P11-P13	D16S159	29	1	0.03	Breast	CR
Unknown	D16S159	22	1	0.05	Liver	CR
Unknown	D16S159	22	1	0.05	Liver	CR
Unknown	Unknown	18	2	0.11	Brain	CR

Chromosome 16 - p Arm

12.2	D16S23	36	5	0.14	Breast	CR
13.2	D16S34	3	1	0.33	Breast	CR
13.2	D16S34	21	7	0.33	Breast	CR
PTER-P13	D16S35	26	4	0.15	Breast	CR
PTER-P13	D16S35	20	4	0.2	Cervix	CR
12-pter	Unknown	18	0	0	Colon	BJC
Unknown	D16S418	22	0	0	Endocrine	CR
Unknown	D16S404	20	2	0.1	Head&Neck	CR
Unknown	D16S404-D16S403-D16S414	22	0	0	Kidney	PNA
Unknown	D16S404-D16S403-D16S414	6	0	0	Kidney	PNA
13.2	D16S34	20	9	0.45	Liver	PNA
13.2	D16S34	8	5	0.62	Liver	CR
13.2	D16S34	6	3	0.5	Liver	CR
PTER-P13	D16S35	7	4	0.57	Liver	CR
PTER-P13	D16S35	24	9	0.38	Liver	PNA
pter-p13	D16S37	2	0	0	Liver	JJC
13.2	D16S34	27	4	0.15	Ovary	JJC
PTER-P13	D16S35	8	0	0	Prostate	PNA
PTER-P13	D16S35	8	0	0	Prostate	CSu
12-pter	Unknown	5	0	0	Stomach	BJC
PTER-P13	D16S35	25	5	0.2	Testis	OJ9
Unknown	D16S291	18	1	0.06	Uterus	CR
SUM		1231	213	0.17		

Chromosome 16 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
16	D16S137	37	5	0.14	Breast	CR 54:513
Unknown	D16S300	23	7	0.3	Breast	GCC 14:171
Unknown	D16S299	36	7	0.19	Breast	GCC 14:171
12.1	D16S304	24	12	0.5	Breast	GCC 14:171
22.1	TAT	43	16	0.37	Breast	CR 54:513
22.1	TAT	41	15	0.37	Breast	GCC 9:101
22.1	TAT	8	5	0.62	Liver	CR 52:1504
22.1	TAT	10	9	0.9	Liver	CR 54:281
22.1	TAT	23	13	0.57	Liver	PNAS 87:6791
22.1	TAT	25	13	0.52	Liver	PNAS 87:6791
22.1	TAT	29	14	0.48	Liver	PNAS 87:6791
Unknown	D16S408	20	3	0.15	Breast	JJCR 86:1054
13	CET	36	9	0.25	Breast	CR 54:513
21	CET	44	20	0.45	Liver	PNAS 87:6791
13-22.1	MT2	36	15	0.42	Liver	PNAS 87:6791
21	D16S151	43	16	0.37	Breast	CR 51:5794
21	D16S151	18	6	0.33	Breast	CR 54:513
21	D16S151	43	8	0.19	Esophageal	GCC 10:177
Unknown	D16S151	8	2	0.25	Liver	CR 51:89
21	D16S265	70	24	0.34	Breast	GCC 9:101
21	D16S265	58	19	0.33	Breast	BCRT 32:5
21	D16S265	19	3	0.16	Ovary	BJC 69:429
22.1	D16S38	35	14	0.4	Breast	CR 54:513
21-22.1	D16S186	28	15	0.54	Breast	GCC 14:171
21-22.1	D16S186	33	13	0.39	Breast	GCC 9:101
21-22.1	D16S186	27	6	0.22	Uterus	CR 54:4294
22.1	D16S318	33	13	0.39	Breast	GCC 9:101
22.1	D16S318	29	14	0.48	Breast	GCC 14:171
Unknown	D16S421	12	2	0.17	Breast	JJCR 86:1054
Unknown	D16S421	27	14	0.52	Breast	GCC 14:171
22.1	D16S4	28	16	0.57	Breast	CR 54:513
22.1	D16S4	29	14	0.48	Breast	GCC 9:101
22.1	D16S4	31	12	0.39	Liver	PNAS 87:6791
22.1	D16S4	9	5	0.56	Liver	CR 52:1504
22.1	D16S4	17	6	0.35	Ovary	CR 53:2393
22.1	D16S152	21	4	0.19	Breast	CR 54:513
22.1	HP	27	11	0.41	Breast	CR 54:513
22.1	HP	21	12	0.57	Breast	CR 51:5794
22.1	HP	29	15	0.52	Breast	GCC 9:101
22.1	HP	9	1	0.11	Cervix	CR 49:3598
22.1	HP	15	3	0.2	Colon	IJC 53:362
Unknown	HP	7	1	0.14	Liver	CR 51:89
Unknown	HP	10	4	0.4	Liver	CR 52:1504
22.1	HP	28	10	0.36	Liver	PNAS 87:6791
22.1	HP	14	8	0.57	Liver	JJCR 81:108
22.1	HP	13	7	0.54	Liver	JJCR 81:108

Chromosome 16 - q Arm

22.1	HP	20	5	0.25	Lung	PN 84:9252
22.1	HP	4	0	0	Neuroblastom a	CR 49:1095
Unknown	HP	24	2	0.08	Ovary	GO 47:137
22.1	HP	22	5	0.23	Ovary	IJC 54:546
22.1	HP	4	0	0	Prostate	G 11:530
Unknown	HP	11	1	0.09	Stomach	CR 52:3099
22.1	HP	10	0	0	Stomach	CR 48:2988
22.1	HP	2	0	0	Testis	CCG 52:72
22.1	HP	2	0	0	Testis	CCG 52:72
22.1	HP	2	0	0	Testis	CCG 52:72
22.1	HP	4	0	0	Uterus	CR 51:5632
22.3-23.2	CTRB	34	9	0.26	Breast	CR 54:513
23.2	CTRB	4	2	0.5	Breast	CR 51:5794
23.2	CTRB	9	5	0.56	Liver	CR 52:1504
22.3-23.2	CTRB	38	17	0.45	Liver	PNAS 87:6391
23.3-24.1	D16S289	28	13	0.46	Breast	GCC 14:171
23.3-24.1	D16S289	57	21	0.37	Breast	GCC 9:101
23.3-24.1	D16S289	22	5	0.23	Uterus	CR 54:4294
24.2	D16S20	45	15	0.33	Breast	CR 54:513
22.1-24	D16S30	6	3	0.5	Breast	CR 54:513
Unknown	D16S511	32	15	0.47	Breast	GCC 14:171
Unknown	D16S402	12	5	0.42	Breast	JJCR 86:1054
Unknown	D16S402	38	20	0.53	Breast	GCC 14:171
Unknown	D16S402	13	2	0.15	Head&Neck	CR 54:1152
24.2-24.3	D16S157	21	9	0.43	Breast	CR 54:513
22-23	D16S157	9	4	0.44	Breast	CR 51:5794
24.2-24.3	D16S43	20	8	0.4	Breast	CR 54:513
Unknown	D16S155	11	2	0.18	Breast	CR 54:513
23-24	D16S156	61	30	0.49	Breast	CR 51:5794
24	APRT	33	17	0.52	Breast	CR 54:513
24	APRT	25	3	0.12	Breast	CR 53:3707
24	APRT	25	3	0.12	Breast	CR 53:4356
24	APRT	19	10	0.53	Breast	GCC 2:191
24	APRT	12	7	0.58	Breast	GCC 9:101
24	APRT	10	6	0.6	Liver	CR 52:1504
24	APRT	26	17	0.65	Liver	PNAS 87:6791
Unknown	D16S7	10	1	0.1	Brain	CR 49:6572
24	D16S7	21	3	0.14	Brain	CR 50:5784
24	D16S7	42	19	0.45	Breast	CR 50:7184
24	D16S7	8	6	0.75	Breast	CR 53:3804
24	D16S7	354	164	0.46	Breast	BJC 71:438
24	D16S7	59	30	0.51	Breast	GCC 9:101
24	D16S7	57	18	0.32	Breast	CR 53:4356
24	D16S7	57	18	0.32	Breast	CR 53:3707
24	D16S7	269	120	0.45	Breast	C 74:2281
24.3	D16S7	68	32	0.47	Breast	CR 54:513

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23-24	D16S7	138	59	0.43	Breast	CR 51:5794
Unknown	D16S7	83	23	0.28	Breast	JJCR 84:1159
Unknown	D16S7	35	1	0.03	Cervix	CR 54:4481
23-24	D16S7	7	2	0.29	Cervix	GCC 9:119
23-24	D16S7	32	6	0.19	Colon	IOC 53:3824
23-24	D16S7	6	1	0.17	Esophageal	CR 51:2113
Unknown	D16S7	15	4	0.27	Esophageal	CR 54:2996
24	D16S7	29	3	0.1	Kidney	CR 51:820
Unknown	D16S7	33	12	0.36	Liver	CR 51:89
24	D16S7	53	24	0.45	Liver	PNAS 87:6791
23-24	D16S7	25	11	0.44	Liver	CR 54:281
24	D16S7	50	14	0.28	Liver	JJCR 84:893
24	D16S7	37	8	0.22	Lung	CR 52:2478
Unknown	D16S7	30	11	0.37	Ovary	CR 51:5118
24	D16S7	3	1	0.33	Pancreas	CR 54:2761
24	D16S7	15	4	0.27	Prostate	PNAS 87:8751
Unknown	D16S7	17	3	0.18	Prostate	BJU 73:390
24	D16S7	32	9	0.28	Sarcoma	CR 52:2419
24	D16S7	43	2	0.05	Testis	O 9:2245
Unknown	D16S7	16	0	0	Uterus	GCC 9:119
24.3	D16S413	41	21	0.51	Breast	GCC 14:171
24.3	D16S413	22	0	0	Endocrine	CR 56:599
24.3	D16S44	10	4	0.4	Breast	CR 54:513
24.3	D16S303	23	11	0.48	Breast	GCC 14:171
24.3	D16S303	42	18	0.43	Breast	GCC 9:101
13	MT2	29	9	0.31	Breast	CR 54:513
13	MT2	8	4	0.5	Liver	CR 52:1504
13	MT2	8	4	0.5	Liver	CR 52:1504
Unknown	D16S10	31	7	0.23	Breast	GCC 9:101
Unknown	D16S260	28	8	0.29	Breast	GCC 9:101
Unknown	D16S266	53	18	0.34	Breast	GCC 9:101
12.1	D16S27	26	7	0.27	Breast	CR 54:513
12.1	D16S27	27	9	0.33	Breast	GCC 9:101
Unknown	D16S301	38	16	0.42	Breast	GCC 9:101
Unknown	D16S305	38	20	0.34	Breast	GCC 9:101
Unknown	D16S320	65	20	0.31	Breast	GCC 9:101
Unknown	D16S398	56	16	0.29	Breast	GCC 9:101
Unknown	D16S5	29	11	0.38	Breast	GCC 9:101
22.1	E-cadherin	28	16	0.57	Breast	GCC 9:101
22.1	E-cadherin	41	27	0.66	Breast	EMBO 14:6107
Unknown	D16S422	21	4	0.19	Head&Neck	CR 54:4756
Unknown	D16S422	20	0	0	Head&Neck	CR 54:4756
Unknown	SPN	22	3	0.14	Head&Neck	CR 54:1152
Unknown	D16S413-D16S402	21	0	0	Kidney	PNAS 92:2854
Unknown	D16S413-D16S402	6	0	0	Kidney	PNAS 92:2854
Unknown	D16S:422-419	6	3	0.5	Kidney	GCC 12:76

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Unknown	Unknown	3	0	0	Liver	BJC 57:1007
Unknown	Unknown	6	0	0	Liver	BJC 64:1083
Unknown	D16S422-419	21	0	0	Melanoma	CR 56:589
Unknown	Unknown	16	5	0.31	Prostate	CSurveys 11:
SUM		4382	1588	0.36		

Chromosome 17 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D17S34	35	5	0.14	Brain	AJP 145:11
13.3	D17S34	82	29	0.35	Breast	AJP 140:21
13.3	D17S34	77	52	0.68	Breast	CR 54:4200
13-TER	D17S34	72	30	0.42	Breast	CGC 76:106
Unknown	D17S34	70	41	0.59	Breast	O 8:781
13.3	D17S34	44	33	0.75	Breast	GCC 4:113
13.3	D17S34	36	22	0.61	Breast	CR 53:1637
Unknown	D17S34	11	6	0.55	Cervix	CGC 79:74
13.3	D17S34	68	34	0.5	Colon	EJC 30A:66
13.3	D17S34	6	5	0.83	Colon	Science Ap 1989:217
13.3	D17S34	6	3	0.5	Head&Neck	AJP 142:11
Unknown	D17S34	12	1	0.08	Head&Neck	CR 52:4787
13.3	D17S34	20	2	0.1	Liver	O 8:497
13.3	D17S34	10	8	0.8	Liver	BJC 64:108
13.3	D17S34	9	4	0.44	Liver	BJC 67:100
13.3	D17S34	23	12	0.52	Ovary	IJC 54:85
13.3	D17S34	20	18	0.9	Ovary	IJC 54:220
Unknown	D17S34	43	18	0.42	Ovary	CR 56:606
13.3	D17S34	11	0	0	Pancreas	CR 54:2761
13.3	D17S34	17	3	0.18	Prostate	CSurveys 1
13.3	D17S34	18	3	0.17	Prostate	PNAS 87:87
13.3	D17S34	7	5	0.71	Sarcoma	CR 53:468
13.3	D17S34	9	0	0	Sarcoma	CR 53:468
13.3	D17S34	10	4	0.4	Sarcoma	CR 53:468
13.3	D17S34	4	2	0.5	Sarcoma	CR 53:468
13.3	D17S34	20	0	0	Testis	GCC 13:249
13.3	D17S849	26	16	0.62	Breast	HMG 4:2047
13.3	D17S926	12	7	0.58	Breast	HMG 4:2047
13.3	D17S30	54	20	0.37	Breast	CR 53:1637
13.3	D17S30	98	57	0.58	Breast	Lan 336:76
13.3	D17S30	59	30	0.51	Breast	JNCI 84:50
13.3	D17S30	52	27	0.52	Breast	PNAS 88:38
13.3	D17S30	51	8	0.16	Breast	HG 91:6
13.3	D17S30	34	16	0.47	Breast	CR 50:7184
13.3	D17S30	33	17	0.52	Breast	ANYAS p 13
13.3	D17S30	3	0	0	Breast	CR 53:2947
13.3	D17S30	6	3	0.5	Cervix	GCC 9:119
13.3	D17S30	39	27	0.69	Colon	CR 50:7166
13.3	D17S30	60	38	0.63	Colon	EJC 30A:66
13.3	D17S30	65	40	0.62	Esophageal	GCC 10:177
13.3	D17S30	51	36	0.71	Head&Neck	O 10:1217
13.3	D17S30	5	2	0.4	Liver	BJC 67:100
13.3	D17S30	26	14	0.54	Liver	CR 51:897
13.3	D17S30	37	23	0.62	Lung	CR 52:2478
13.3	D17S30	16	4	0.25	Melanoma	GCC 7:169

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13.3	D17S30	14	9	0.64	Ovary	CR 50:2724
13.3	D17S30	21	19	0.86	Ovary	IJC 54:85
13.3	D17S30	46	37	0.8	Ovary	CR 56:606
13.3	D17S30	41	27	0.66	Ovary	O 7:1059
13.3	D17S30	7	0	0	Prostate	GCC 11:119
13.3	D17S30	3	0	0	Sarcoma	CR 53:468
13.3	D17S30	6	4	0.67	Sarcoma	CR 53:468
13.3	D17S30	3	0	0	Sarcoma	CR 53:468
13.3	D17S30	6	0	0	Sarcoma	CR 53:468
13.3	D17S30	17	16	0.94	Sarcoma	CR 49:6247
13.3	D17S30	15	3	0.2	Uterus	GCC 9:119
13.3	D17S28	11	4	0.36	Brain	CR 49:6572
13.3	D17S28	22	3	0.14	Brain	AJP 145:11
13.3	D17S28	12	4	0.33	Brain	CR 49:6572
13.3	D17S28	27	11	0.41	Breast	CR 54:6270
13.3	D17S28	62	15	0.24	Breast	GCC 76:106
13.3	D17S28	37	26	0.7	Breast	CR 54:4200
13.3	D17S28	11	4	0.36	Breast	HMG 4:2047
13.3	D17S28	23	12	0.52	Breast	CR 53:1637
13.3	D17S28	27	4	0.15	Cervix	CR 54:4481
13.3	D17S28	14	1	0.07	Cervix	BJC 67:71
13.3	D17S28	7	5	0.71	Colon	Science Ap 1989:217
13.3	D17S28	13	8	0.62	Colon	GCC 3:468
13.3	D17S28	12	4	0.33	Colon	CCG 48:167
13.3	D17S28	2	0	0	Head&Neck	CR 52:4787
13.3	D17S28	11	0	0	Kidney	JU 150:129
13.3	D17S28	3	1	0.33	Liver	CR 53:368
13.3	D17S28	3	3	1	Lung	CR 49:5130
13.3	D17S28	16	2	0.12	Ovary	IJC 52:575
13.3	D17S28	8	6	0.75	Ovary	CR 50:2724
13.3	D17S28	23	15	0.65	Ovary	CR 56:606
13.3	D17S28	6	4	0.67	Ovary	IJC 54:85
13.3	D17S28	18	14	0.78	Ovary	IJC 54:220
13.3	D17S28	3	1	0.33	Pancreas	CR 54:2761
13.3	D17S28	3	0	0	Pancreas	GCC 3:468
13.3	D17S28	10	2	0.2	Stomach	BJC 59:150
13.3	D17S28	7	0	0	Stomach	HG 89:445
13.3	D17S28	29	12	0.41	Testis	O 9:2245
13.3	D17S28	1	1	1	Uterus	CR 51:5632
Unknown	Unknown	20	10	0.5	Bladder	JU 153:109
Unknown	Unknown	76	21	0.28	Brain	CR 56:164
13.3	D17S34-S5	13	7	0.54	Brain	CR 54:1397
13.3	D17S34-S5	20	11	0.55	Brain	CR 54:1397
13.3	D17S5	22	4	0.18	Brain	AJP 145:11
13.3	D17S5	16	6	0.38	Brain	IJC 63:372
13.3	D17S5	13	6	0.46	Brain	CR 49:6572

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13.3	D17S5	11	6	0.55	Brain	CR 49:6572
13.3	Unknown	74	20	0.27	Breast	AJP 140:721
13.3	D17S5	62	26	0.42	Breast	JJCR 84:11
13.3	D17S5	68	37	0.54	Breast	O 8:781
13.3	D17S5	57	28	0.49	Breast	BCRT 28:23
13.3	D17S5	4	2	0.5	Breast	CR 53:4804
13.3	D17S5	29	16	0.55	Breast	GCC 2:191
13.3	D17S5	50	8	0.16	Breast	CR 43:4356
13.3	D17S5	465	224	0.48	Breast	BJC 71:438
13.3	D17S5	34	15	0.44	Breast	HMC 4:2047
13.3	D17S5	82	53	0.65	Breast	CR 54:4200
13.3	D17S5	75	21	0.28	Breast	CGC 76:106
13.3	D17S5	354	174	0.49	Breast	C 74:2281
13.3	D17S5	39	19	0.46	Breast	IJC 53:41
13.3	D17S5	42	25	0.6	Breast	IJC 50:528
13.3	D17S5	40	22	0.55	Breast	GCC 4:1132
13.3	D17S5	125	63	0.5	Breast	CR 51:5794
13.3	D17S5	61	26	0.43	Breast	BG 90:635
13.3	D17S5	52	27	0.52	Breast	PNAS 88:38
13.3	D17S5	15	4	0.27	Cervix	CGC 79:74
13.3	D17S5	12	1	0.08	Cervix	BJC 67:71
13.3	D17S5	32	5	0.16	Cervix	CR 54:4481
13.3	Unknown	7	6	0.86	Colon	Science Ap 1989:217
13.3	D17S5	35	24	0.69	Colon	BJC 59:750
13.3	D17S5	19	7	0.37	Colon	CCG 48:167
13.3	D17S5	5	3	0.6	Colon	O 9:991
13.3	D17S5	27	21	0.78	Colon	IJC 53:382
13.3	D17S5	17	7	0.41	Colon	GCC 3:468
13.3	D17S5	26	10	0.38	Colon	S 241:961
13.3	D17S54-S5	24	11	0.46	Esophageal	CR 52:6525
13.3	D17S5	22	10	0.45	Esophageal	CR 51:2113
13.3	Unknown	6	5	0.83	Head&Neck	AJP 142:11
13.3	D17S5	11	2	0.18	Head&Neck	CR 52:1494
13.3	D17S5	48	8	0.17	Kidney	CR 51:5817
13.3	D17S5	23	6	0.26	Kidney	JU 150:129
13.3	D17S5	15	5	0.33	Kidney	CR 51:820
13.3	D17S5	31	5	0.16	Kidney	CR 51:1544
13.3	D17S5	15	1	0.07	Kidney	CR 51:1071
13.3	D17S5	2	1	0.5	Kidney	CR 51:1544
13.3	D17S5	20	3	0.15	Liver	O 6:491
13.3	D17S5	14	3	0.21	Liver	CR 51:4367
13.3	D17S5	31	15	0.48	Liver	CR 53:368
13.3	D17S5	9	3	0.33	Liver	BJC 64:108
13.3	D17S54-S5	11	11	1	Lung	CR 49:5130
13.3	D17S5	6	6	1	Lung	CR 55:28
13.3	D17S54-S5	38	25	0.66	Ovary	O 7:2069

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13.3	D17S34-S5	6	2	0.33	Ovary	O 7:2069
13.3	D17S5	17	13	0.76	Ovary	IJC 54:220
13.3	D17S5	28	12	0.43	Ovary	CR 51:5118
13.3	D17S5	13	9	0.27	Ovary	IJC 54:516
13.3	D17S5	34	7	0.21	Ovary	IJC 52:575
13.3	D17S5	41	27	0.66	Ovary	O 7:1059
13.3	D17S5	28	15	0.54	Ovary	GO 47:137
13.3	D17S5	5	0	0	Pancreas	GCC 3:468
13.3	D17S5	8	0	0	Pancreas	BJC 65:809
13.3	D17S5	4	2	0.5	Pancreas	CR 54:2361
13.3	D17S5	27	1	0.04	Pediatric	CR 50:3279
13.3	D17S5	8	6	0.75	Sarcoma	CGC 53:43
13.3	D17S5	22	16	0.73	Sarcoma	CR 52:2419
13.3	D17S5	60	38	0.63	Stomach	IA 57:238
13.3	D17S5	38	19	0.5	Stomach	CR 51:2926
13.3	D17S5	14	2	0.14	Stomach	GCC 3:468
13.3	D17S5	24	9	0.38	Stomach	HG 92:244
13.3	D17S5	30	6	0.2	Testis	O 9:2245
13.3	D17S5	9	4	0.44	Uterus	CR 51:5632
13.3	D17S379	22	15	0.58	Ovary	CR 55:606
13.3	ABR	29	6	0.21	Ovary	CR 56:606
Unknown	D17S65	16	10	0.62	Breast	CR 54:4200
13	D17S65	16	11	0.69	Breast	GE 5:554
13	D17S65	2	2	1	Colon	S:April 16
13	D17S1	15	3	0.2	Brain	AJP 145:11
13	D17S1	15	2	0.13	Brain	AJP 145:11
13	D17S1	21	4	0.19	Breast	HG 91:6
13	D17S1	20	9	0.45	Breast	GCC 2:191
13	D17S1	29	9	0.31	Breast	CR 53:4356
13	D17S1	7	2	0.29	Cervix	CR 49:3598
13	D17S1	14	6	0.43	Colon	CR 50:7166
13	D17S1	9	0	0	Colon	N 331:275
13	D17S1	2	2	1	Colon	S:April 16
13	D17S1	12	4	0.33	Colon	S 241:961
13	D17S1	30	13	0.43	Head&Neck	O 10:1217
13	D17S1	7	1	0.14	Liver	JJCR 81:10
13	D17S1	11	2	0.18	Liver	CR 53:368
13	D17S1	3	1	0.33	Lung	PNAS 86:50
13	D17S1	9	8	0.89	Lung	PNAS 86:50
13	D17S1	17	8	0.47	Lung	PN 84:9252
13	D17S1	7	7	1	Lung	CR 49:5130
13	D17S1	11	2	0.18	Lung	PNAS 86:50
13	D17S1	4	0	0	Neuroblastom	CR 49:1095
13	D17S1	5	0	0	Sarcoma	CR 53:468
13	D17S1	3	1	0.33	Sarcoma	CR 53:468
13	D17S1	3	0	0	Sarcoma	CR 53:468

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13	D17S1	8	7	0.88	Sarcoma	CR 52:2419
13	D17S1	2	0	0	Sarcoma	CR 52:468
13	D17S1	13	12	0.92	Sarcoma	CR 49:6247
13	D17S1	5	4	0.2	Stomach	CR 42:1099
13	D17S1	10	0	0	Stomach	CR 48:2988
13	D17S1	6	1	0.17	Uterus	CR 51:5732
Unknown	D17S796	17	0	0	Endocrine	CR 56:599
Unknown	D17S796	41	14	0.34	Head&Neck	CR 57:1756
Unknown	D17S796	33	0	0	Head&Neck	CR 54:4756
Unknown	D17S796	6	0	0.5	Kidney	GC 302:96
Unknown	D17S796	32	5	0.16	Melanoma	CR 56:589
12.0-13	D17S906	19	13	0.16	Prostate	GC 313:278
13.1	D17S31	9	2	0.22	Brain	CR 49:6572
13.1	D17S31	7	2	0.15	Brain	HP 34:471
13.1	D17S31	8	4	0.5	Brain	CR 49:6572
13.1	D17S31	21	7	0.33	Breast	HG 97:267
13.1	D17S31	54	24	0.44	Breast	Lan 336:76
13.1	D17S31	31	22	0.65	Breast	CR 51:2200
13.1	D17S31	87	37	0.43	Breast	CR 51:5794
13.1-11.2	D17S31	25	11	0.44	Breast	IJC 50:528
13.1	D17S31	2	1	0.5	Breast	CR 52:2947
13.1	D17S31	11	1	0.09	Cervix	BJC 67:77
13.1-11.2	D17S31	16	7	0.44	Colon	CR 50:7166
13.1	D17S31	6	6	1	Colon	S:Apr 11:16
13.1	D17S31	15	9	0.6	Esophageal	CR 54:2996
13.1	D17S31	29	18	0.62	Head&Neck	O 10:1217
13.1-11.2	D17S31	28	5	0.18	Kidney	CR 51:5817
13.1	D17S31	25	0	0	Kidney	JU 150:129
13.1-11.2	D17S31	16	6	0.38	Liver	CR 51:89
13.1	D17S31	21	12	0.57	Liver	CR 53:968
13.1	D17S31	17	7	0.41	Ovary	IJC 54:546
13.1	D17S31	7	2	0.29	Ovary	IJC 54:85
13.1	D17S31	11	8	0.73	Ovary	IJC 54:220
13.1	D17S31	7	4	0.57	Ovary	BJC 65:40
13.1	D17S31	6	2	0.33	Ovary	CR 56:606
13.1	D17S31	3	1	0.33	Pancreas	CR 54:2761
13.1-11.2	D17S31	17	12	0.71	Sarcoma	CR 52:2419
13.1	D17S31	15	15	1	Sarcoma	CR 49:6247
13.1	D17S31	12	9	0.75	Sarcoma	CR 52:2419
13.1	TP53	7	0	0	Bladder	HG 97:455
13.1	TP53	21	9	0.43	Brain	CR 54:1397
Unknown	TP53	1	0	0	Brain	AJP 145:11
13.1	TP53	45	6	0.13	Brain	O 6:1313
13.1	TP53	6	2	0.33	Brain	CR 49:6572
13.1	TP53	22	9	0.41	Brain	CGC 74:139
13.1	TP53	38	11	0.29	Brain	CR 52:1427

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13.1	TP53	15	7	0.47	Brain	CR 54:1397
13.1	TP53	6	2	0.33	Brain	CR 44:492
13.1	TP53	31	22	0.71	Breast	BJC 68:64
Unknown	TP53	63	17	0.27	Breast	BCRT 28:23
13.1	TP53	61	14	0.23	Breast	CGC 76:106
Unknown	TP53	19	6	0.32	Breast	CR 51:6194
13.1	TP53	44	28	0.64	Breast	HG 90:635
13.1	TP53	35	13	0.37	Breast	IJC 30:528
13.1	TP53	70	26	0.37	Breast	CR 51:5794
13.1	TP53	65	13	0.22	Breast	JCR 38:47
Unknown	TP53	11	6	0.55	Breast	CR 52:2624
13.1	TP53	81	22	0.27	Breast	Jan 336:76
13.1	TP53	25	10	0.4	Breast	GCC 4:113
13.1	TP53	36	10	0.28	Breast	BJC 63:254
13.1	TP53	12	5	0.42	Breast	CR 53:2947
13.1	TP53	110	72	0.65	Breast	CR 54:4200
13.1	TP53	36	15	0.42	Breast	CR 53:1637
13.1	TP53	17	9	0.53	Breast	GCC 4:113
13.1	TP53	41	34	0.83	Breast	IJC 57:498
Unknown	TP53	16	0	0	Cervix	CGC 79:74
13.1	TP53	9	1	0.11	Cervix	BJC 67:71
Unknown	TP53	6	3	0.5	Cervix	GCC 9:119
13.1	TP53	21	5	0.24	Cervix	CR 54:4481
13.1	TP53	17	8	0.47	Colon	CR 52:741
13.1	TP53	6	5	0.83	Colon	GAST 107:3
Unknown	TP53	23	15	0.65	Colon	EJC 30A:26
Unknown	TP53	48	38	0.79	Colon	O 8:1391
Unknown	TP53	26	22	0.85	Colon	GAS 103:16
13.1	TP53	30	17	0.57	Colon	GAST 104:1
Unknown	TP53	6	4	0.67	Colon	O 9:991
13.1	TP53	25	12	0.48	Colon	HP 25:1069
13.1	TP53	14	8	0.57	Colon	CR 50:7166
13.1	TP53	17	8	0.47	Colon	JNCI 84:11
13.1	TP53	17	7	0.41	Colon	JNCI 84:11
13.1	TP53	17	10	0.59	Colon	IJC 53:382
13.1	TP53	25	14	0.56	Colon	CR 52:3965
13.1	TP53	12	10	0.83	Colon	CR 51:4436
13.1	TP53	27	15	0.56	Esophageal	C 73:2472
13.1	TP53	14	10	0.71	Esophageal	C 71:1933
Unknown	TP53	47	27	0.57	Esophageal	CR 52:6525
13.1	TP53	14	7	0.5	Head&Neck	CR 54:1152
Unknown	TP53	32	14	0.44	Head&Neck	O 9:2077
13.1	TP53	27	15	0.56	Head&Neck	C 73:2472
13.1	TP53	39	21	0.54	Head&Neck	O 10:1217
13.1	TP53	20	4	0.2	Kidney	CR 51:5817
Unknown	TP53	40	5	0.12	Kidney	BJC 69:230

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13.1	TP53	2	0	0	Kidney	GCC 12:76
13.1	TP53	10	6	0.6	Kidney	IJC 64:999
13.1	TP53	16	3	0.19	Kidney	CR 51:820
Unknown	TP53	65	9	0.14	Leukemia	B 86:4587
13.1	TP53	50	14	0.28	Liver	JJCR 84:89
13.1	TP53	7	6	0.86	Liver	CR 51:6920
Unknown	TP53	4	1	0.25	Liver	CARC 17:14
13.1	TP53	64	17	0.58	Liver	C 73:42
Unknown	TP53	19	11	0.58	Liver	CR 54:281
13.1	TP53	5	1	0.2	Liver	O 8:2903
13.1	TP53	7	3	0.43	Liver	CR 51:89
13.1	TP53	24	17	0.71	Lung	CR 54:5643
13.1	TP53	57	21	0.37	Lung	O 10:937
13.1	TP53	7	5	0.71	Lung	CR 51:5849
13.1	TP53	3	2	0.67	Lung	CR 54:5643
13.1	TP53	3	0	0	Melanoma	GCC 74:169
Unknown	TP53	28	7	0.25	Melanoma	BJC 69:253
13.1	TP53	42	19	0.45	Ovary	CR 56:606
13.1	TP53	12	5	0.42	Ovary	IJC 54:546
13.1	TP53	18	10	0.56	Ovary	BJC 69:40
13.1	TP53	9	6	0.67	Ovary	IJC 54:85
13.1	TP53	9	2	0.22	Ovary	IJC 52:575
13.1	TP53	23	18	0.78	Ovary	IJC 54:220
13.1	TP53	18	12	0.67	Ovary	BJC 69:429
13.1	TP53	12	3	0.25	Ovary	CR 51:5118
13.1	TP53	20	16	0.8	Ovary	CR 51:5171
Unknown	TP53	35	26	0.74	Ovary	BJC 72:883
13.1	TP53	7	1	0.14	Ovary	O 7:2069
13.1	TP53	2	1	0.5	Ovary	O 7:2069
13.1	TP53	32	18	0.56	Ovary	O 7:2069
13.1	TP53	13	3	0.23	Ovary	O 7:2069
13.1	TP53	7	5	0.71	Pancreas	GCC 15:157
13.1	TP53	27	3	0.11	Prostate	AJP 145:28
13.1	TP53	8	3	0.38	Prostate	JU 151:107
13.1	TP53	4	0	0	Prostate	AJP 147:11
Unknown	TP53	5	3	0.6	Sarcoma	CR 53:468
Unknown	TP53	4	1	0.25	Sarcoma	CR 53:468
Unknown	TP53	7	1	0.14	Sarcoma	CR 53:468
Unknown	TP53	12	6	0.5	Sarcoma	CR 53:468
Unknown	TP53	63	23	0.37	Stomach	LI 72:232
13.1	TP53	16	5	0.31	Stomach	CGC 75:45
Unknown	TP53	5	1	0.2	Testis	GCC 6:92
13.1	TP53	7	3	0.43	Testis	O 9:2245
13.1	TP53	9	2	0.22	Uterus	GCC 9:119
13.1	TP53	3	1	0.33	Uterus	CR 51:5632
13.1	TP53	4	1	0.25	Uterus	CR 51:5632

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Unknown	TP53	28	3	0.11	Uterus	CR 54:4294
13.1	D17S286	27	1	0.15	Cervix	CR 56:1397
13.1	D17S786	2	0	0	Kidney	GCC 12:76
12	D17S520	14	7	0.5	Brain	CR 54:1397
12	D17S520	20	13	0.65	Brain	CR 54:1397
13.1	D17S520	31	15	0.48	Head&Neck	O 9:2077
12	D17S520	19	11	0.58	Ovary	BJC 69:429
13.1	D17S520	26	2	0.08	Uterus	CR 54:4294
13.1	MYH2	10	5	0.5	Brain	CR 49:6572
13.1	MYH2	8	2	0.25	Brain	CR 49:6572
13.1	MYH2	14	1	0.07	Brain	AJP 145:11
13.1	MYH2	14	10	0.71	Colon	IJC 53:382
13.1	MYH2	5	2	0.4	Liver	CR 53:368
13.1	MYH2	10	2	0.2	Liver	GCC 48:82
13.1	MYH2	14	3	1	Lung	CR 49:5130
13.1	MYH2	15	12	0.21	Ovary	IJC 51:116
13.1	MYH2	17	6	0.8	Sarcoma	CR 49:6247
13.1	MYH2	19	8	0.5	Sarcoma	CR 52:2619
13.1	MYH2	19	8	0.42	Stomach	CR 52:3099
12	D17S67	8	4	0.3	Uterus	CR 51:5632
12	D17S67	35	22	0.5	Brain	AJP 145:11
12	D17S67	12	11	0.63	Breast	CR 54:4200
12	D17S67	1	1	0.92	Breast	GE 5:554
12	D17S67	22	10	1	Colon	Science Ap 1989:217
12	D17S67	16	7	0.45	Ovary	IJC 54:546
13.1	EW505	3	2	0.46	Ovary	CR 56:606
13.1	UC 10-41	4	3	0.67	Colon	Science Ap 1989:217
13.1	EW401	3	1	0.78	Colon	Science Ap 1989:217
13.1	EW402	2	1	0.33	Colon	Science Ap 1989:217
13.1	EW405	3	1	0.5	Colon	Science Ap 1989:217
13.1	D17S29	15	1	0.33	Colon	Science Ap 1989:217
13.1	D17S29	9	1	0.07	Brain	CR 49:6572
13.1	D17S29	2	0	0.11	Brain	CR 49:6572
13.1	CHRNA1	26	14	0	Colon	Science Ap 1989:217
13.1	CHRNA1	22	8	0.54	Head&Neck	O 9:2077
13.1	CHRNA1	28	14	0.36	Head&Neck	CR 54:1132
11.2-12	D17S261	6	2	0.5	Ovary	CR 56:606
11.2-12	D17S261	7	3	0.33	Brain	CR 54:1397
11.2-12	D17S261	19	8	0.43	Brain	CR 54:1397
12-11.2	D17S71	15	2	0.42	Leukemia	B 83:3449
				0.13	Brain	AJP 145:11

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12-11.2	D17S71	3	2	0.67	Breast	GE 5:554
12-11.2	D17S71	18	15	0.83	Colon	IJC 53:382
12-11.2	D17S71	3	1	0.43	Bladder	CR 53:568
12-11.2	D17S71	10	10	1	Lung	CR 49:5130
12-11.2	D17S71	31	7	0.54	Ovary	GO 55:254
12-11.2	D17S71	20	11	0.55	Ovary	GO 47:137
12-11.2	D17S71	12	6	0.5	Sarcoma	CR 52:2419
12-11.2	D17S71	9	5	0.56	Sarcoma	CR 52:2419
12-11.2	D17S71	13	5	0.38	Ovary	CR 53:562
13.1	D17S122	23	4	0.17	Brain	AJP 145:11
13.1	D17S122	29	11	0.38	Head&Neck	HMG 4:2047
13.1	D17S122	12	7	0.58	Head&Neck	CR 54:1152
Unknown	D17S58	17	2	0.12	Brain	AJP 145:11
11.2-11.1	D17S58	21	7	0.33	Breast	GE 5:554
11.2-11.1	D17S58	63	35	0.56	Breast	CR 53:562
Unknown	D17S58	35	14	0.4	Breast	O 8:781
11.2-11.1	D17S58	10	1	0.1	Cervix	HMG 4:2047
11.2-11.1	D17S58	5	1	0.2	Colon	Science Ap 1989:217
Unknown	D17S58	9	0	0	Head&Neck	CR 52:4787
11.2-11.1	D17S58	11	9	0.82	Ovary	IJC 54:85
Unknown	D17S58	19	12	0.63	Ovary	CR 56:606
Unknown	D17Z1	27	1	0.04	Breast	GE 5:554
Unknown	D17Z1	27	1	0.04	Breast	GE 5:554
D17S5-D17S58	Unknown	21	8	0.38	Bladder	CR 51:5405
Unknown	CHRNBI-TP53	30	18	0.6	Bladder	CR 55:5213
Unknown	Unknown	32	13	0.41	Brain	CR 50:5784
12-11.2	D17S121	17	3	0.18	Brain	AJP 145:11
Unknown	D17S5:28-31	14	0	0	Brain	CGC 73:122
Unknown	D17S5:28-31	25	6	0.24	Brain	CGC 73:122
Unknown	D17S5:28-31	15	5	0.33	Brain	CGC 73:122
Unknown	D17S66	15	2	0.13	Brain	AJP 145:11
13.3	Unknown	28	10	0.36	Breast	HMG 4:2047
13	Unknown	51	17	0.33	Breast	Lan 336:76
13.3	Unknown	27	16	0.59	Breast	HMG 4:2047
13.3	Unknown	22	9	0.41	Breast	HMG 4:2047
13.1-13.3	Unknown	88	38	0.43	Breast	CR 51:5794
13.1	Unknown	16	6	0.38	Breast	CR 53:1637
13.3	Unknown	21	7	0.33	Breast	HMG 4:2047
13.3	D17S1174	7	3	0.43	Breast	HMG 4:2047
13	D17S513	17	6	0.35	Breast	CR 53:2947
Unknown	D17S66	7	0	1	Breast	CR 54:4200
13	Unknown	15	0	0	Cervix	BJC 67:71
13.3	Unknown	1	1	1	Colon	S:April 16
13.3	Unknown	3	3	1	Colon	S:April 16
13.3	Unknown	1	1	1	Colon	S:April 16
13.3	Unknown	4	4	1	Colon	S:April 16

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13.1	Unknown	2	2	1	Colon	Science 2p
Unknown	HF-12	12	6	0.5	Colon	JNCI 84:11
13	D17S513	32	20	0.62	Esophageal	C 73:2472
13	D17S513	32	20	0.62	Head&Neck	C 73:2472
13	D17S513	32	6	0.75	Head&Neck	C 73:2472
13.2	CI17-732	35	1	0.03	Kidney	BJC 69:230
Unknown	D17S849-D17S796	6	0	0	Kidney	PNAS 92:28
Unknown	D17S849-D17S796	21	1	0.05	Kidney	PNAS 92:28
Unknown	D17S786-799	23	4	0.17	Leukemia	CR 55:577
Unknown	Unknown	30	28	0.93	Lung	CR 54:2322
13	Unknown	19	10	0.53	Ovary	BJC 65:40
Unknown	D17S1-D17S28	15	2	0.13	Ovary	IJC 54:546
13.1	D17S260	21	10	0.48	Ovary	CR 55:546
13.1-13.3	D17S34-D17S28- D17S5-D17S379- P53-D17S513	7	7	1	Ovary	AJHG 55:66
13.1-13.3	D17S34-D17S28- D17S5-D17S379- P53-D17S513	2	2	1	Ovary	AJHG 55:66
13.1-13.3	D17S34-D17S28- D17S5-D17S379- P53-D17S513	12	12	1	Ovary	AJHG 55:66
13.1-13.3	D17S34-D17S28- D17S5-D17S379- P53-D17S513	1	1	1	Ovary	AJHG 55:66
Unknown	D17S5-34-71- MYH2	36	29	0.81	Ovary	CR 53:2393
13	D17S513	36	16	0.44	Ovary	CR 56:606
13.3	D17S578	29	12	0.41	Ovary	CR 56:606
13.3	D17S654	27	17	0.63	Ovary	CR 56:606
13.3	D17S695	41	18	0.44	Ovary	CR 56:606
Unknown	D17S34-5-28-31	19	12	0.63	Ovary	CGC 85:43
Unknown	TP53-D17S:515- 520-513	18	9	0.5	Ovary	BJC 72:133
Unknown	D17S1-D17S28	7	0	0	Prostate	G 11:530
12.0-13	D17S1149	15	4	0.27	Prostate	GCC 13:278
Unknown	D17S1-D17S28	8	2	0.25	Stomach	GCC 3:468
Unknown	Unknown	19	2	0.11	Testis	G 5:134
Unknown	D17S134	17	0	0	Testis	GCC 13:249
Unknown	D17S30-D17S787	24	2	0.08	Testis	LI 73:606
Unknown	12G6	22	2	0.09	Uterus	CR 54:4294
SUM		10343	4539	0.44		

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Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	D17S146	6	4	0.67	Ovary	IJC 54:220
11.2-12	D17S33	8	1	0.12	Brain	CR 49:6572
11.2-12	D17S33	9	0	0	Brain	CR 49:6572
11.2-12	D17S33	59	13	0.22	Breast	CR 51:5794
11.2-12	D17S33	7	1	0.14	Ovary	CR 51:5794
11.2-12	D17S33	7	2	0.29	Sarcoma	CR 52:2419
11.2-12	D17S33	9	2	0.22	Sarcoma	CR 52:2419
11.2-12	CRYB1	13	0	0	Brain	AJP 145:1175
11.2-12	CRYB1	28	2	0.07	Breast	GCC 4:115
11.2-12	CRYB1	16	0	0	Colon	JNCI 84:1100
Unknown	D17S117	15	6	0.4	Breast	CR 53:5617
Unknown	D17S73	25	6	0.24	Breast	O 8:781
CEN-12	D17S73	27	10	0.37	Breast	CR 53:5617
CEN-12	D17S73	7	3	0.43	Ovary	IJC 54:85
11.2-12	D17S907	18	1	0.06	Prostate	GCC 13:278
11.2-12	THRA1	37	10	0.27	Breast	CR 54:2549
11.2-12	THRA1	66	17	0.26	Breast	GCC 11:58
11.2-12	THRA1	14	11	0.79	Breast	CR 52:2624
11.2-12	THRA1	17	7	0.41	Breast	AJOG 172:908
11.2-12	THRA1	13	5	0.38	Esophageal	CL 97:129
11.2-12	THRA1	17	12	0.71	Ovary	AJOG 172:908
11.2-12	THRA1	20	1	0.05	Ovary	IJC 54:220
13.1	TCF2	26	7	0.27	Head&Neck	O 9:2077
21.1	RARA	11	6	0.55	Ovary	IJC 54:85
11.2-12	D17S250	1	0	0	Bladder	HG 94:231
21	D17S250	5	1	0.2	Breast	CR 54:6069
21	D17S250	81	17	0.21	Breast	CR 54:2549
21	D17S250	78	18	0.23	Breast	GCC 11:58
11.2-12	D17S250	26	5	0.19	Breast	O 8:781
11.2-12	D17S250	6	1	0.17	Breast	HG 94:231
11.2-12	D17S250	14	7	0.5	Breast	CR 52:2624
21	D17S250	11	2	0.18	Esophageal	CL 97:129
11.2-12	D17S250	19	5	0.26	Head&Neck	CR 54:1152
11.2-12	D17S250	2	0	0	Ovary	HG 94:231
11.2-12	D17S250	22	14	0.64	Ovary	BGC 69:429
11.2-12	D17S250	20	2	0.1	Prostate	O 11:1241
21	D17S250	20	2	0.1	Prostate	CR 55:1002
21	PHB	4	3	0.75	Ovary	IJC 54:85
Unknown	PHB	9	9	1	Ovary	IJC 54:220
21	D17S800	1	0	0	Bladder	HG 94:231
21	D17S800	7	6	0.86	Breast	CR 54:6069
21	D17S800	4	0	0	Breast	HG 94:231
21	D17S902	37	10	0.27	Breast	CR 54:2549
21	D17S902	16	4	0.25	Prostate	GCC 13:278
21	D17S579	1	0	0	Bladder	HG 94:231
21	D17S579	19	11	0.58	Breast	CR 52:2624

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21	D17S579	7	5	0.71	Breast	CR 54:6069
21	D17S579	34	7	0.21	Breast	O 8:781
21	D17S579	85	20	0.24	Breast	GCC 11:58
21	D17S579	16	5	0.31	Breast	AJOG 172:908
21	D17S579	94	12	0.13	Breast	CR 54:2549
21	D17S579	4	1	0.25	Breast	HG 94:231
21	D17S579	52	21	0.1	Breast	BCRT 32:1
21	D17S579	14	4	0.29	Esophageal	CL 97:129
21	D17S579	26	8	0.31	Head&Neck	CR 54:1152
21	D17S579	17	13	0.76	Ovary	AJOG 172:908
21	D17S579	23	9	0.39	Ovary	GO 55:215
21	D17S579	2	0	0	Ovary	HG 94:231
21	D17S579	18	14	0.18	Ovary	IJC 54:220
21	D17S579	37	22	0.59	Ovary	CR 56:606
21	D17S579	9	11	0.14	Ovary	IJC 54:85
21	D17S579	20	2	0.1	Prostate	CR 55:1002
21	D17S579	20	2	0.1	Prostate	O 11:1241
21	D17S579	25	0	0	Uterus	CR 54:4294
Unknown	D17S509	75	18	0.24	Breast	CR 53:4356
Unknown	D17S509	26	3	0.12	Breast	HG 91:6
Unknown	D17S509	11	5	0.45	Liver	CR 51:89
21	HOX2	19	1	0.05	Prostate	O 11:1241
Unknown	PPY	20	5	0.25	Breast	CR 53:5617
Unknown	D17S806	26	2	0.08	Cervix	CR 56:197
21.3-22	COL1A1	24	10	0.42	Breast	O 8:781
22	D17S41	43	21	0.49	Breast	CR 53:5617
12.0-24	D17S41	20	8	0.4	Breast	O 8:781
22	D17S41	11	7	0.64	Ovary	IJC 54:85
12.0-24	D17S41	20	5	0.25	Ovary	IJC 54:546
12.0-24	D17S41	8	7	0.88	Ovary	IJC 54:220
21.3-22	NM23	23	6	0.26	Breast	GCC 14:113
21.3-22	NM23	61	8	0.13	Breast	ANYAS p.137
21.3-22	NM23	29	3	0.1	Colon	CR 54:3979
21.3-22	NM23	17	3	0.18	Colon	EJC 30A:664
21.3-22	NM23	7	0	0	Melanoma	GCC 7:169
21.3-22	NM23	20	13	0.65	Ovary	IJC 54:85
21.3-22	NM23	23	2	0.09	Stomach	IJC 84:184
21.3-22	NM23	7	0	0	Uterus	C 73:1686
Unknown	NME1	55	25	0.45	Breast	CR 53:5617
Unknown	NME1	68	20	0.29	Breast	GCC 11:58
Unknown	NME1	17	5	0.29	Breast	CR 52:2624
Unknown	NME1	45	10	0.22	Breast	BCRT 28:231
Unknown	NME1	48	7	0.15	Breast	IJC 84:1159
Unknown	NME1	18	1	0.06	Cervix	CR 54:4481
Unknown	NME1	27	2	0.07	Esophageal	C 73:2472
Unknown	NME1	27	2	0.07	Head&Neck	C 73:2472

Chromosome 17 - q Arm

Unknown	NME1	17	1	0.8	Ovary	CR 51:224
Unknown	NME1	21	1	0.05	Prostate	JU 151:1073
Unknown	NME1	21	1	0.05	Prostate	O 9:2245
Unknown	NME1	18	8	0.44	Testis	O 9:2245
Unknown	D17S74	18	7	0.05	Breast	CR 53:3382
22	D17S74	50	10	0.2	Breast	BCRT 28:231
22	D17S74	58	22	0.05	Breast	CR 53:3382
22	D17S74	67	13	0.19	Breast	HG 91:6
Unknown	D17S74	32	2	0.08	Breast	CR 53:3382
22	D17S74	106	49	0.46	Breast	CR 54:4200
Unknown	D17S74	49	29	0.01	Breast	CR 53:3382
23	D17S74	49	12	0.24	Breast	CR 53:3382
Unknown	D17S74	76	22	0.05	Breast	CR 53:3382
Unknown	D17S74	57	10	0.18	Breast	JJCR 84:1159
23	D17S74	52	20	0.07	Esophageal	CR 53:3382
Unknown	D17S74	54	20	0.37	Esophageal	GCC 10:177
Unknown	D17S74	28	5	0.07	Esophageal	CR 53:3382
Unknown	D17S74	30	3	0.1	Kidney	CR 51:820
Unknown	D17S74	21	21	0.05	Liver	CR 53:3382
Unknown	D17S74	12	2	0.17	Liver	CR 53:3382
22	D17S74	7	7	0.05	Lung	CR 49:5130
22	D17S74	9	8	0.89	Lung	PN 86:5099
22	D17S74	3	1	0.05	Lung	PN 86:5099
22	D17S74	11	2	0.18	Lung	PN 86:5099
Unknown	D17S74	39	8	0.21	Lung	CR 52:2479
Unknown	D17S74	24	10	0.42	Ovary	IJC 54:546
Unknown	D17S74	23	16	0.07	Ovary	IJC 54:220
Unknown	D17S74	26	10	0.38	Ovary	CR 51:5118
23	D17S74	6	0	0	Ovary	CR 53:3382
23	D17S74	8	1	0.12	Ovary	CR 53:3382
22	D17S74	10	2	0.2	Ovary	IJC 52:575
23	D17S74	17	6	0.35	Ovary	CR 53:3382
23	D17S74	16	2	0.2	Ovary	CR 53:3382
22	D17S74	17	12	0.71	Ovary	IJC 54:85
Unknown	D17S74	18	4	0.22	Sarcoma	CR 49:6247
Unknown	D17S74	22	3	0.14	Sarcoma	CR 52:2419
Unknown	MPO	11	4	0.36	Breast	CR 52:2624
Unknown	MPO	31	5	0.16	Head&Neck	O 9:2077
Unknown	MPO	20	1	0.05	Prostate	O 11:3241
Unknown	D17S86	44	9	0.2	Breast	CR 53:5617
21-12-21.1	C117-24	36	13	0.36	Esophageal	CR 54:1638
12-21.1	C117-316	37	11	0.3	Breast	CR 53:3382
12-21.1	C117-316	32	9	0.28	Esophageal	CR 54:1638
12-21.1	C117-316	13	6	0.46	Ovary	CR 53:3382
12-21.1	C117-316	1	0	0	Ovary	CR 53:3382
12-21.1	C117-316	9	1	0.11	Ovary	CR 53:3382

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12-21.1	CI17-316	3	0	0	Ovary	CR 53:3382
21.3	CI17-477	32	22	0.69	Esophageal	CR 54:1638
21.3	CI17-28	7	3	0.43	Esophageal	CR 54:1638
21.3	CI17-28	26	15	0.58	Esophageal	CR 54:1638
21.3	CI17-592	18	8	0.44	Breast	CR 53:3382
21.3	CI17-592	17	6	0.35	Esophageal	CR 54:1638
21.3	CI17-592	4	2	0.5	Ovary	CR 53:3382
21.3	CI17-592	1	0	0	Ovary	CR 53:3382
21.3	CI17-592	3	2	0.67	Ovary	CR 53:3382
21.3	CI17-592	1	0	0	Ovary	CR 53:3382
21.3	CI17-701	138	48	0.35	Breast	CR 53:3382
21.3	CI17-701	38	21	0.55	Esophageal	CR 54:1638
21.3	CI17-701	12	5	0.42	Ovary	CR 53:3382
21.3	CI17-701	7	0	0	Ovary	CR 53:3382
21.3	CI17-701	15	9	0.6	Ovary	CR 53:3382
21.3	CI17-701	12	2	0.17	Ovary	CR 53:3382
21.3	CI17-730	96	36	0.38	Breast	CR 53:3382
21.3	CI17-730	35	20	0.57	Esophageal	CR 54:1638
21.3	CI17-730	4	0	0	Ovary	CR 53:3382
21.3	CI17-730	4	0	0	Ovary	CR 53:3382
21.3	CI17-730	12	6	0.5	Ovary	CR 53:3382
21.3	CI17-730	4	2	0.5	Ovary	CR 53:3382
21.3	CI17-507	25	7	0.28	Breast	CR 53:3382
21.3	CI17-507	18	10	0.56	Esophageal	CR 54:1638
21.3	CI17-507	3	1	0.33	Ovary	CR 53:3382
21.3	CI17-507	5	2	0.4	Ovary	CR 53:3382
21.3	CI17-507	7	6	0.86	Ovary	CR 53:3382
21.3	CI17-507	3	1	0.33	Ovary	CR 53:3382
21.3	CI17-533	93	25	0.27	Breast	CR 53:3382
21.3	CI17-533	42	21	0.5	Esophageal	CR 54:1638
21.3	CI17-533	9	4	0.44	Ovary	CR 53:3382
21.3	CI17-533	9	3	0.33	Ovary	CR 53:3382
21.3	CI17-533	11	6	0.55	Ovary	CR 53:3382
21.3	CI17-533	7	1	0.14	Ovary	CR 53:3382
21-23	D17S78	14	0	0	Brain	AJP 145:1175
21-23	D17S78	25	5	0.2	Ovary	IJC 54:546
22-24	GH	39	13	0.33	Breast	O 8:781
22-24	GH	16	4	0.25	Breast	CR 52:2624
22-24	GH	59	13	0.22	Breast	CR 53:5617
22-24	GH	12	1	0.08	Lung	CR 49:5130
22-24	GH	14	7	0.5	Ovary	GO 55:245
22-24	GH	15	1	0.07	Uterus	CR 51:5632
Unknown	66 E6	11	4	0.36	Breast	O 8:781
23-24	D17S40	23	10	0.43	Breast	CR 53:5617
Unknown	D17S40	14	5	0.36	Breast	O 8:781
23-24	D17S40	15	9	0.6	Ovary	IJC 54:85

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Unknown	D17S40	18	4	0.22	Ovary	IJC 54:546
23-qter	D17S21	15	0	0	Brain	AJP 145:1175
23-qter	D17S21	20	7	0.35	Breast	CR 53:5617
23-qter	D17S21	25	13	0.52	Ovary	IJC 54:546
Unknown	D17S515	32	6	0.19	Head&Neck	O 9:2077
Unknown	D17S801	32	4	0.12	Cervix	CR 56:197
Unknown	D17S785	37	1	0.03	Head&Neck	CR 54:4756
Unknown	D17S785	37	16	0.43	Head&Neck	CR 54:4756
Unknown	D17S785	6	3	0.5	Kidney	GCC 12:76
Unknown	D17S785	27	1	0.04	Melanoma	CR 56:589
Unknown	CACNLB1	19	2	0.11	Prostate	O 11:1241
Unknown	D17S20	72	5	0.07	Breast	CR 53:5617
23-25.5	D17S4	9	0	0	Brain	CR 49:6572
23-25.5	D17S4	14	3	0.21	Brain	CR 49:6572
23-25.5	D17S4	34	1	0.03	Brain	AJP 145:1175
23-25.5	D17S4	47	6	0.13	Breast	HG 91:6
23-25.4	D17S4	42	18	0.43	Breast	BJC 69:754
23-25.3	D17S4	51	21	0.41	Breast	CR 54:4200
23-25.3	D17S4	34	10	0.29	Breast	IJC 53:11
23-25.3	D17S4	104	28	0.27	Breast	CR 51:5794
23-25.3	D17S4	63	24	0.38	Breast	CR 53:5617
23-25.3	D17S4	34	10	0.29	Breast	GCC 4:113
23-25.5	D17S4	47	16	0.34	Breast	Lan 336:761
23-25.3	D17S4	36	7	0.19	Breast	ANYAS p.137
23-25.5	D17S4	35	3	0.09	Cervix	CR 54:4481
23-25	D17S4	13	0	0	Cervix	BJC 67:71
23-25.3	D17S4	20	3	0.15	Colon	JNCI 84:1100
23-25.3	D17S4	23	0	0	Colon	CCG 48:167
23-25.5	D17S4	25	5	0.2	Colon	CR 50:7166
23-25.5	D17S4	14	1	0.07	Esophageal	CR 51:2113
23-25.3	D17S4	23	7	0.3	Esophageal	CR 54:2996
23-25.5	D17S4	14	1	0.07	Kidney	CR 51:1071
23-25.5	D17S4	8	2	0.25	Liver	CR 53:368
23-25.3	D17S4	5	0	0	Liver	PNAS 86:8852
23-25.3	D17S4	2	0	0	Lung	CR 49:5130
23-25.3	D17S4	16	11	0.69	Ovary	O 7:2069
23-25.3	D17S4	16	2	0.12	Ovary	O 7:2069
23-25.3	D17S4	41	30	0.73	Ovary	O 7:2069
23-25.3	D17S4	7	4	0.57	Ovary	Unknown
23-25.3	D17S4	29	11	0.38	Ovary	IJC 54:546
23-25.3	D17S4	21	2	0.1	Ovary	CR 51:5118
23-25.3	D17S4	30	11	0.37	Ovary	IJC 52:575
23-25	D17S4	15	10	0.67	Ovary	IJC 54:85
23-25.5	D17S4	15	10	0.67	Ovary	IJC 54:85
23-25.3	D17S4	19	12	0.63	Ovary	IJC 54:220
23-25	D17S4	4	0	0	Pancreas	CR 54:2761

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23-25	D17S4	11	0	0	Prostate	GCC 11:119
23-25	D17S4	9	2	0.22	Sarcoma	CR 52:2419
23-25.5	D17S4	12	9	0.75	Sarcoma	CR 52:2419
23-25.3	D17S4	14	3	0.21	Sarcoma	CR 49:6247
23-25	D17S4	7	0	0	Stomach	CR 51:2926
23-25.5	D17S4	42	17	0.4	Testis	O 9:2245
23-25.3	TK1	21	1	0.05	Breast	CR 53:5617
23-qter	D17S77	31	2	0.06	Brain	AJP 145:1175
23-qter	D17S77	30	11	0.37	Breast	CR 53:5617
Unknown	D17S26	9	0	0	Breast	CR 53:5617
Unknown	D17S26	16	5	0.31	Ovary	CR 50:2724
23-25	D17S75	71	23	0.32	Breast	CR 51:5794
23-25.3	D17S24	23	0	0	Brain	AJP 145:1175
Unknown	D17S24	34	12	0.35	Breast	GCC 4:113
Unknown	D17S24	59	27	0.46	Breast	CR 53:5617
Unknown	D17S24	59	20	0.34	Breast	O 8:781
23-25.3	D17S24	40	17	0.42	Breast	CR 54:4200
23-25	D17S24	42	10	0.24	Breast	CR 51:5794
23-25.3	D17S24	40	17	0.42	Breast	CR 54:4200
23-25.3	D17S24	20	8	0.4	Breast	GCC 2:191
23-25.3	D17S24	4	2	0.5	Breast	CR 53:3804
Unknown	D17S24	21	2	0.1	Colon	JNCI 84:1100
23-25.3	D17S24	18	11	0.61	Ovary	IJC 54:85
Unknown	D17S24	16	8	0.5	Ovary	IJC 54:546
23-25.3	D17S24	18	11	0.61	Ovary	IJC 54:85
23-25	D17S24	3	0	0	Ovary	CR 51:5118
Unknown	D17S24	9	1	0.11	Prostate	G 11:530
23-25	D17S27	17	6	0.35	Breast	CR 51:5794
Unknown	D17S79	9	2	0.22	Breast	CR 53:5617
Unknown	D17S79	9	2	0.22	Breast	CR 53:5617
Unknown	D17S587	1	0	0	Bladder	HG 94:231
12.0-21	D17S588	1	0	0	Bladder	HG 94:231
Unknown	Unknown	28	3	0.11	Brain	CR 50:5784
25.1	Unknown	31	9	0.29	Breast	CR 53:3382
23	Unknown	31	10	0.32	Breast	CR 53:3382
22	Unknown	41	14	0.34	Breast	CR 53:3382
25.3	Unknown	45	13	0.29	Breast	CR 53:3382
21	D173700	54	10	0.19	Breast	CR 54:2549
21	D17S1184	11	2	0.18	Breast	CR 54:6069
21	D17S1322	11	10	0.91	Breast	CR 54:6069
21	D17S1325	11	11	1	Breast	CR 54:6069
21	D17S1328	6	5	0.83	Breast	CR 54:6069
21	D17S183	36	8	0.22	Breast	CR 54:2549
Unknown	D17S2	4	0	0	Breast	GCC 2:191
Unknown	D17S293	15	3	0.2	Breast	AJOG 172:908
Unknown	D17S308	23	9	0.39	Breast	O 8:781

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Unknown	D17S5-D17S1-D17S31-D17S509-D17S74-D17S4	75	18	0.24	Breast	CR 53:3707
Unknown	D17S587	6	1	0.17	Breast	HG 94:231
12.0-21	D17S588	9	2	0.22	Breast	O 8:781
12.0-21	D17S588	6	1	0.17	Breast	HG 94:231
12.0-21	D17S588	17	8	0.47	Breast	AJOG 172:908
21	D17S648	39	7	0.18	Breast	CR 54:2549
Unknown	D17S68	23	16	0.7	Breast	CR 54:4200
21	D17S702	92	21	0.23	Breast	CR 54:2549
Unknown	D17S702	80	24	0.3	Breast	GCC 11:58
Unknown	D17S733	65	18	0.28	Breast	GCC 11:58
21	D17S746	36	10	0.28	Breast	CR 54:2549
21	D17S750	59	14	0.24	Breast	CR 54:2549
23-qter	D17S77	30	11	0.37	Breast	CR 53:5617
Unknown	D17S773	9	2	0.22	Breast	CR 53:5617
21	D17S776	10	6	0.6	Breast	CR 54:6069
21	D17S776	70	17	0.24	Breast	GCC 11:58
21	D17S776	63	19	0.3	Breast	CR 54:2549
21	D17S846	74	24	0.32	Breast	CR 54:2549
21	D17S855	30	8	0.27	Breast	CR 54:2549
21	D17S855	86	21	0.24	Breast	GCC 11:58
21	D17S855	10	8	0.8	Breast	CR 54:6069
21	D17S856	53	10	0.19	Breast	CR 54:2549
21	D17S857	68	17	0.25	Breast	CR 54:2549
21	D17S859	17	2	0.12	Breast	CR 54:2549
21	D17S870	441	173	0.39	Breast	BJC 71:438
21	D17S870-C117-730	289	98	0.34	Breast	C 74:2281
Unknown	EDH17B-HSD-A3T	19	7	0.37	Breast	GCC 11:58
Unknown	EDH17B-HSD-DEL	20	9	0.45	Breast	GCC 11:58
Unknown	EPB3	15	6	0.4	Breast	CR 53:5617
21	GAS	50	13	0.26	Breast	CR 54:2549
Unknown	PROH1B	6	1	0.17	Cervix	GCC 9:119
Unknown	D17S791	22	1	0.05	Endocrine	CR 56:599
25.3	Unknown	40	11	0.28	Esophageal	CR 54:1638
22	Unknown	33	16	0.48	Esophageal	CR 54:1638
25.1	Unknown	26	14	0.54	Esophageal	CR 54:1638
Unknown	D17S874	35	20	0.57	Esophageal	GCC 10:177
Unknown	GP3A	15	6	0.4	Head&Neck	O 9:2077
12.0-21	D17S588	34	2	0.06	Kidney	BJC 69:230
Unknown	D17S802-805-809	22	5	0.23	Leukemia	CR 55:5377
Unknown	D17S32	13	0	0	Liver	CR 53:368
25.3	Unknown	7	3	0.43	Ovary	CR 53:3382
22	Unknown	3	1	0.33	Ovary	CR 53:3382
25.1	Unknown	7	0	0	Ovary	CR 53:3382
25.1	Unknown	17	6	0.35	Ovary	CR 53:3382
22	Unknown	3	0	0	Ovary	CR 53:3382

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25.3	Unknown	8	3	0.38	Ovary	CR 53:3382
25.3	Unknown	8	4	0.5	Ovary	CR 53:3382
22	Unknown	5	4	0.8	Ovary	CR 53:3382
25.3	Unknown	6	0	0	Ovary	CR 53:3382
22	Unknown	1	0	0	Ovary	CR 53:3382
23	Unknown	3	0	0	Ovary	CR 53:3382
23	Unknown	5	5	1	Ovary	CR 53:3382
25.1	Unknown	11	6	0.55	Ovary	CR 53:3382
25.1	Unknown	10	1	0.1	Ovary	CR 53:3382
23	Unknown	2	0	0	Ovary	CR 53:3382
23	Unknown	8	3	0.38	Ovary	CR 53:3382
Unknown	46E6-HOX2B-D17S250-588-579	18	10	0.56	Ovary	BJC 72:1330
Unknown	D17S136	6	5	0.83	Ovary	IJC 54:220
Unknown	D17S174	10	8	0.8	Ovary	IJC 54:220
Unknown	D17S180	6	4	0.67	Ovary	IJC 54:220
Unknown	D17S250-579-588-NM23-GH	120	64	0.53	Ovary	CR 53:1218
12.0-21	D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588	3	2	0.67	Ovary	AJHG 55:666
12.0-21	D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588	14	12	0.86	Ovary	AJHG 55:666
12.0-21	D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588	11	8	0.73	Ovary	AJHG 55:666
12.0-21	D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588	1	1	1	Ovary	AJHG 55:666
Unknown	D17S293	11	9	0.82	Ovary	IJC 54:220
Unknown	D17S293	18	14	0.78	Ovary	AJCG 172:908
Unknown	D17S308	17	14	0.82	Ovary	IJC 54:220
Unknown	D17S587	2	0	0	Ovary	HG 94:231
12.0-21	D17S588	11	6	0.55	Ovary	BJC 69:429
12.0-21	D17S588	20	14	0.7	Ovary	AJCG 172:908
12.0-21	D17S588	2	0	0	Ovary	HG 94:231
Unknown	D17S73-41-4-77	37	28	0.76	Ovary	CR 53:2393
22-23	NME1-D17S74-GH-D17S40-D17S4-D17S75	11	11	1	Ovary	AJHG 55:666
22-23	NME1-D17S74-GH-D17S40-D17S4-D17S75	3	3	1	Ovary	AJHG 55:666

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22-23	NME1-D17S74-GH- D17S40-D17S4- D17S75	1	1	1	Ovary	AJHG 55:666
22-23	NME1-D17S74-GH- D17S40-D17S4- D17S75	14	14	1	Ovary	AJHG 55:666
Unknown	D17S1323	12	3	0.25	Prostate	O 11:1241
Unknown	D17S1327	15	2	0.13	Prostate	O 11:1241
12.0-21	D17S588	19	2	0.11	Prostate	CR 55:1002
12.0-21	D17S588	19	2	0.11	Prostate	O 11:1241
21.3	D17S752	14	1	0.07	Prostate	GCC 13:278
21	D17S776	12	5	0.42	Prostate	O 11:1241
21	D17S846	19	2	0.11	Prostate	O 11:1241
21	D17S855	18	8	0.44	Prostate	O 11:1241
21	D17S855	18	8	0.44	Prostate	CR 55:1002
21	D17S856	15	5	0.33	Prostate	O 11:1241
21	D17S856	15	6	0.4	Prostate	CR 55:1002
21	D17S857	20	2	0.1	Prostate	O 11:1241
21	D17S859	18	1	0.06	Prostate	O 11:1241
Unknown	KRT9	18	2	0.11	Prostate	O 11:1241
Unknown	D17S32	10	1	0.1	Sarcoma	CR 49:6247
Unknown	D17S32	14	2	0.14	Sarcoma	CR 52:2419
Unknown	D17S293	19	0	0	Uterus	CR 54:4294
Unknown	PROHIB	2	1	0.5	Uterus	GCC 9:119
SUM		9605	3006	0.31		

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Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
11.2-12.1	TTR	18	9	0.5	Colon	IJC 53:382
11.1-11.2	D18S7	5	2	0.4	Breast	CR 53:3804
11.1-11.2	D18S7	7	2	0.29	Colon	S 241:961
11.1-11.2	D18S7	9	2	0.22	Stomach	HG 92:244
11.1-11.2	D18S7	17	8	0.47	Stomach	CR 52:3099
Unknown	D18S1	7	1	0.14	Breast	GCC 2:191
Unknown	D18S1	8	4	0.5	Colon	IJC 53:382
Unknown	D18S1	11	0	0	Colon	N 331:273
Unknown	D18S1	16	4	0.25	Colon	CR 50:7166
Unknown	D18S1	1	1	1	Lung	PNAS 86:5099
Unknown	D18S1	5	2	0.4	Lung	PNAS 86:5099
Unknown	D18S1	4	1	0.25	Lung	PNAS 86:5099
Unknown	D18S1	9	3	0.33	Ovary	O 7:1059
Unknown	D18S1	15	7	0.47	Sarcoma	CR 52:2419
Unknown	D18S1	6	2	0.33	Uterus	CR 51:5632
11	D18S6	8	2	0.25	Bladder	BJC 70:697
11	D18S6	12	2	0.17	Breast	PNAS 87:7737
11-pter	D18S6	24	5	0.21	Breast	JNCI 84:506
11	D18S6	16	6	0.38	Cervix	CR 54:4481
11	D18S6	19	9	0.47	Colon	CR 50:7166
11	D18S6	6	0	0	Colon	CCG 48:167
11	D18S6	17	3	0.18	Ovary	IJC 54:546
11	D18S6	1	0	0	Prostate	JU 151:1073
11	D18S6	15	4	0.27	Testis	O 9:2245
11	D18S6	5	1	0.2	Testis	GCC 13:249
Unknown	D18S57	33	10	0.3	Cervix	CR 56:197
Unknown	D18S22	14	2	0.14	Brain	CR 50:5784
Unknown	D18S22	17	3	0.18	Breast	GCC 2:191
Unknown	D18S22	29	11	0.38	Esophageal	CR 54:2996
Unknown	D18S22	11	7	0.64	Sarcoma	CR 52:2419
21.3	D18S8	7	3	0.43	Breast	CR 53:3804
21.3	D18S8	27	9	0.33	Colon	S 241:961
21.3	D18S8	7	5	0.71	Stomach	CR 52:3099
21.3	D18S8	14	6	0.43	Stomach	HG 92:244
Unknown	D18S24	13	1	0.08	Breast	CR 50:7166
Unknown	D18S24	6	0	0	Cervix	GCC 9:119
Unknown	D18S24	4	0	0	Kidney	CR 51:820
Unknown	D18S24	17	4	0.24	Lung	CR 52:2478
Unknown	D18S24	8	0	0	Ovary	CR 51:5118
Unknown	D18S24	3	0	0	Uterus	GCC 9:119
11.2-12.1	PALB	18	9	0.5	Colon	CR 50:7166
11.2-12.1	PALB	11	2	0.18	Colon	GCC 3:468
11.2-12.1	PALB	6	0	0	Pancreas	GCC 3:468
11.2-12.1	PALB	8	2	0.25	Stomach	GCC 3:468
11.2-12.1	PALB	3	0	0	Uterus	CR 51:5632
21.3	DCC	28	8	0.29	Bladder	CR 55:5213

Chromosome 18 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
11.21-PTER	D18S40	25	3	0.12	Uterus	CR 54:4294
Unknown	Unknown	12	1	0.08	Brain	CR 50:5784
Unknown	D18S16	22	0	0	Breast	CR 53:4356
11.3	D18S3	9	1	0.11	Breast	CR 50:7184
Unknown	D18S53	31	8	0.26	Cervix	CR 56:197
Unknown	D18S59	20	1	0.05	Endocrine	CR 56:599
Unknown	D18S21	20	2	0.1	Esophageal	CR 54:2996
Unknown	D18S21	15	1	0.07	Esophageal	CR 51:2113
Unknown	D18S3	18	2	0.11	Esophageal	GCC 10:177
11.21-PTER	D18S40	22	6	0.27	Head&Neck	CR 54:1152
Unknown	D18S59	13	0	0	Head&Neck	CR 54:4756
Unknown	D18S59	18	3	0.17	Head&Neck	CR 54:4756
11.3	D18S3	12	0	0	Kidney	CR 51:820
Unknown	D18S59	21	0	0	Kidney	PNAS 92:2854
Unknown	D18S59	6	1	0.17	Kidney	PNAS 92:2854
Unknown	D18S54	19	1	0.05	Leukemia	CR 55:5377
11.3	D18S3	16	4	0.25	Lung	CR 52:2478
Unknown	D18S59	33	4	0.12	Melanoma	CR 56:589
11.3	D18S3	6	0	0	Ovary	CR 51:5118
11.21-PTER	D18S40	15	4	0.27	Ovary	BJC 72:1330
Unknown	D18S6	10	1	0.1	Ovary	CR 53:2393
11.3	D18S3	15	0	0	Prostate	G 11:530
Unknown	D18S21	10	2	0.2	Sarcoma	CR 52:2419
11.21-PTER	D18S40	25	3	0.12	Uterus	CR 54:4294
SUM		388	45	0.12		

Chromosome 18 - q Arm

21.3	DCC	15	8	0.53	Bladder	BJC 70:697
21.3	DCC	26	2	0.08	Breast	CR 53:4356
21.3	DCC	16	5	0.31	Breast	BJC 68:64
21	DCC	5	1	0.2	Cervix	BJC 67:71
21.3	DCC	12	3	0.25	Cervix	BJC 67:71
21.3	DCC	48	18	0.38	Colon	EJC 30A:664
21.3	DCC	25	13	0.52	Colon	CR 54:3979
21.3	DCC	4	1	0.25	Colon	O 9:991
21.3	DCC	41	29	0.71	Colon	S 247:45
21.3	DCC	19	0	0	Endocrine	GCC 13:9
21.3	DCC	44	10	0.23	Esophageal	CR 54:3007
21.3	DCC	50	12	0.24	Esophageal	CR 52:6525
21.3	DCC	5	1	0.2	Kidney	GCC 12:76
21.3	DCC	19	11	0.58	Leukemia	B 83:3449
21.3	DCC	26	8	0.31	Leukemia	B 82:927
21.3	DCC	9	3	0.33	Leukemia	B 82:927
21.3	DCC	11	1	0.09	Liver	CR 51:85
21.3	DCC	6	2	0.33	Ovary	BJC 71:462
21.3	DCC	34	15	0.44	Ovary	O 7:1059
21.3	DCC	7	3	0.43	Ovary	O 7:1059
21.3	DCC	2	2	1	Pancreas	CR 54:2761
21	DCC	12	2	0.17	Prostate	PNAS 87:8751
21.3	DCC	11	5	0.45	Prostate	CR 53:2723
21.3	DCC	13	5	0.38	Prostate	GCC 11:119
21.3	DCC	12	2	0.17	Prostate	CSurveys 11:1
21	DCC	7	5	0.71	Stomach	CR 52:3099
21.3	DCC	18	5	0.28	Stomach	L1 74:835
21.3	DCC	10	5	0.5	Stomach	CR 52:3099
21.3	DCC	51	17	0.33	Uterus	CR 54:4294
21.3	DCC	8	1	0.12	Uterus	CR 51:5632
21.3	DCC	5	1	0.2	Uterus	CR 51:5633
21.2-21.3	D18S35	22	0	0	Uterus	CR 54:4294
21.3	BCL2	14	1	0.07	Breast	PNAS 87:7737
21.3	BCL2	10	6	0.6	Colon	JJCR 85:584
21.3	BCL2	20	10	0.5	Ovary	O 7:1059
21.3	BCL2	7	2	0.29	Prostate	GCC 11:119
21.3	BCL2	17	4	0.24	Stomach	JJCR 85:584
Unknown	D18S68	23	8	0.35	Cervix	CR 56:197
Unknown	D18S19	22	9	0.41	Breast	PNAS 87:7737
Unknown	D18S19	8	3	0.38	Prostate	GCC 11:119
21.3-qter	D18S5	9	4	0.44	Bladder	BJC 70:697
12	D18S5	17	4	0.24	Bladder	CR 51:5405
21.3-qter	D18S5	70	11	0.16	Breast	JJCR 84:1159
12	D18S5	5	1	0.2	Breast	GCC 2:191
21.3-qter	D18S5	43	6	0.14	Breast	AJP 140:215
21.3-qter	D18S5	16	11	0.69	Breast	PNAS 87:7737

Chromosome 18 - q Arm

21.3-qter	D18S5	21	2	0.1	Cervix	CR 54:4481
12	D18S5	7	0	0	Cervix	CR 49:3598
21.3-qter	D18S5	6	2	0.33	Colon	O 9:991
21.3-qter	D18S5	21	16	0.76	Colon	IJC 53:382
12	D18S5	19	12	0.63	Colon	CR 50:7166
12	D18S5	29	11	0.38	Esophageal	GCC 10:177
12	D18S5	19	1	0.05	Kidney	CR 51:1544
12	D18S5	18	1	0.06	Liver	JJCR 81:108
12	D18S5	28	3	0.11	Lung	PN 84:9252
12	D18S5	7	0	0	Neuroblastom a	CR 49:1095
21.3-qter	D18S5	16	4	0.25	Ovary	IJC 54:546
21.3-qter	D18S5	15	9	0.6	Ovary	O 7:1059
21.3-qter	D18S5	21	12	0.57	Prostate	JO 151:1073
21.3-qter	D18S5	16	4	0.25	Prostate	GCC 11:119
12	D18S5	13	0	0	Stomach	CR 48:2988
21.3-qter	D18S5	15	10	0.67	Stomach	CR 52:3099
21.3-qter	D18S5	16	1	0.07	Testis	GCC 13:249
12	D18S5	42	16	0.38	Testis	O 9:2245
12	D18S5	9	2	0.22	Uterus	CR 51:5632
Unknown	D18S58-D18S61	6	1	0.17	Kidney	PNAS 92:2854
Unknown	D18S58-D18S61	22	0	0	Kidney	PNAS 92:2854
23	D18S11	67	17	0.25	Breast	PNAS 87:7737
23	D18S11	8	3	0.38	Colon	GCC 3:468
23	D18S11	25	8	0.32	Ovary	IJC 54:546
23	D18S11	35	21	0.6	Ovary	O 7:1059
23	D18S11	5	0	0	Pancreas	GCC 3:468
23	D18S11	13	2	0.15	Prostate	GCC 11:119
23	D18S11	13	2	0.15	Stomach	GCC 3:468
Unknown	D18S70	41	0	0	Head&Neck	CR 54:4756
Unknown	D18S70	43	3	0.07	Head&Neck	CR 54:4756
Unknown	D18S70	21	0	0	Kidney	PNAS 92:2854
Unknown	D18S70	6	1	0.17	Kidney	PNAS 92:2854
Unknown	D18S70	23	5	0.22	Melanoma	CR 56:589
Unknown	D18S70	23	5	0.22	Melanoma	CR 56:589
12.1-21.1	Unknown	18	4	0.22	Bladder	BJC 70:697
23	Unknown	11	4	0.36	Bladder	BJC 70:697
Unknown	D18S22	12	0	0	Brain	CR 49:6572
Unknown	D18S46	17	1	0.06	Endocrine	CR 56:599
Unknown	D18S34	26	6	0.23	Head&Neck	CR 54:1152
Unknown	D18S:58-67	23	4	0.17	Leukemia	CR 55:5377
Unknown	Unknown	2	0	0	Liver	BJC 67:1007
Unknown	Unknown	5	0	0	Liver	BJC 64:1083
Unknown	GCC-D18S34	28	12	0.43	Ovary	CR 53:2393
Unknown	MBP- D18S:34-35	15	6	0.4	Ovary	BJC 72:1330
Unknown	PLANH2	7	2	0.29	Ovary	O 7:1059
Unknown	Unknown	6	4	0.67	Pancreas	CR 54:2761

Chromosome 18 - q Arm

Unknown	Unknown	1	0	0	Pancreas	CR 54:2761
Unknown	Unknown	6	0	0	Pancreas	BJC 65:809
23	Unknown	2	2	1	Prostate	GU 151:1073
Unknown	D18S31	19	2	0.11	Testis	GCC 13:249
Unknown	JOSR4.4	20	5	0.25	Testis	O 9:2245
SUM		2301	659	0.29		

Chromosome 19 - p Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
Unknown	LIPE	21	0	0	Uterus	CR 54:4294
13.2-CEN	D19S11	36	2	0.06	Brain	AJP 145:1175
Unknown	D19S20	12	0	0	Brain	CR 50:5784
Unknown	D19S20	35	1	0.03	Brain	AJP 145:1175
Unknown	D19S20	8	0	0	Brain	CR 49:6572
13.2	D19S24	15	0	0	Brain	AJP 145:1175
12-13.2	D19S76	14	0	0	Brain	CR 54:1397
12-13.2	D19S76	11	1	0.09	Brain	CR 54:1397
13.2-13.1	LDLR	3	1	0.33	Brain	CR 54:1397
13.2-13.1	LDLR	11	0	0	Brain	CR 54:1397
13.2-CEN	D19S11	26	7	0.27	Breast	CR 53:4356
Unknown	D19S20	36	7	0.19	Breast	CR 50:7184
13.3-.2	D19S22	35	1	0.03	Breast	CR 53:4356
13.2-CEN	D19S11	45	1	0.02	Cervix	CR 54:4481
13.3	D19S177	27	4	0.15	Cervix	CR 56:197
Unknown	D19S20	8	0	0	Cervix	GCC 9:119
Unknown	D19S221	29	7	0.24	Cervix	CR 56:197
Unknown	D19S7	26	4	0.15	Cervix	CR 54:4481
Unknown	D19S216	22	1	0.05	Endocrine	CR 56:599
Unknown	D19S20	22	6	0.27	Esophageal	CR 54:2996
Unknown	D19S20	25	2	0.08	Esophageal	GCC 10:177
13.3-.2	D19S22	34	11	0.32	Esophageal	GCC 10:177
13.3	D19S177	16	4	0.25	Head&Neck	CR 54:1152
Unknown	D19S216	15	0	0	Head&Neck	CR 54:4756
Unknown	D19S216	19	1	0.05	Head&Neck	CR 54:4756
Unknown	D19S221	19	6	0.32	Head&Neck	CR 54:1152
13.3	Unknown	48	7	0.15	Kidney	CR 51:5817
Unknown	D19S20	40	8	0.2	Kidney	CR 51:5817
Unknown	D19S20	25	8	0.32	Kidney	CR 51:520
13.3	D19S21	30	3	0.1	Kidney	CR 51:5817
Unknown	D19S216	3	0	0	Kidney	PNAS 92:2854
Unknown	D19S216	17	1	0.06	Kidney	PNAS 92:2854
13.2-TER	C3	3	0	0	Liver	CCG 48:72
13.3-.2	D19S22	28	1	0.04	Liver	CR 51:89
Unknown	D19S7	11	0	0	Liver	JJCR 81:108
Unknown	D19S20	26	3	0.12	Lung	CR 52:2478
Unknown	D19S7	17	0	0	Lung	PN 84:9252
Unknown	D19S216	25	2	0.08	Melanoma	CR 56:589
Unknown	Unknown	19	5	0.26	Ovary	CR 51:5118
13.2-CEN	D19S11	16	3	0.19	Ovary	IJC 54:546
13.2-CEN	D19S11	13	2	0.16	Ovary	CR 53:2393
13.3	D19S177	11	5	0.45	Ovary	EJC 69:429
Unknown	D19S20	13	5	0.38	Ovary	GO 55:198
Unknown	D19S20	24	8	0.33	Ovary	CR 51:5118
13.3-13.2	INSR	21	5	0.24	Ovary	IJC 54:546
13.3-.2	D19S22	6	0	0	Pancreas	CR 54:2761

Chromosome 19 - p Arm

13.2-CEN	D19S11	3	0	0	Prostate	G 11:530
Unknown	D19S20	21	5	0.24	Sarcoma	CR 52:2419
Unknown	D19S7	3	1	0.33	Sarcoma	CR 52:2419
13.2-CEN	D19S11	46	2	0.04	Testis	O 9:2245
Unknown	D19S20	20	1	0.05	Testis	LT 73:606
Unknown	D19S20	20	1	0.05	Testis	G 5:134
13.3-13.2	INSR	2	0	0	Testis	CCG 52:72
13.3-13.2	INSR	3	0	0	Testis	CCG 52:72
13.3-13.2	INSR	1	0	0	Testis	CCG 52:72
Unknown	D19S20	14	0	0	Uterus	GCC 9:119
Unknown	LIFE	21	0	0	Uterus	CR 54:4294
SUM		1099	143	0.13		

Chromosome 19 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
13.2	APOC2	11	0	0	Uterus	CR 54:4294
13.2	APOC2	33	19	0.58	Brain	AJP 145:1175
13.2	APOC2	22	8	0.36	Brain	CR 54:1397
13.2	APOC2	15	1	0.07	Brain	CR 54:1397
13.1-13.2	BCI3	5	4	0.8	Brain	CR 54:1397
13.1-13.2	BCI3	6	1	0.17	Brain	CR 54:1397
13.3	CKM	34	19	0.56	Brain	AJP 145:1175
13.2	CYP2	24	13	0.54	Brain	AJP 145:1175
13.2	D19S178	12	1	0.08	Brain	CR 54:1397
13.2	D19S178	18	5	0.28	Brain	CR 54:1397
13.4	D19S180	21	9	0.43	Brain	CR 54:1397
13.4	D19S180	11	2	0.18	Brain	CR 54:1397
13.1	D19S191	23	6	0.26	Brain	CR 54:1397
13.1	D19S191	12	2	0.17	Brain	CR 54:1397
13.4	D19S22	18	1	0.06	Brain	CR 50:5784
13.4	D19S22	37	18	0.49	Brain	AJP 145:1175
12-13.1	D19S30	15	7	0.47	Brain	AJP 145:1175
12-13.1	D19S31	6	4	0.67	Brain	AJP 145:1175
13.1	D19S32	21	10	0.48	Brain	AJP 145:1175
13.1-13.2	D19S47	18	4	0.22	Brain	CR 54:1397
13.1-13.2	D19S47	11	2	0.18	Brain	CR 54:1397
12-13.1	D19S49	22	5	0.23	Brain	CR 54:1397
12-13.1	D19S49	12	1	0.08	Brain	CR 54:1397
13.3	D19S51	12	7	0.58	Brain	AJP 145:1175
13.3	D19S62	12	7	0.58	Brain	AJP 145:1175
13.3	D19S63	24	15	0.62	Brain	AJP 145:1175
12	D19S7	21	10	0.48	Brain	AJP 145:1175
11-CEN	D19S74	7	4	0.57	Brain	AJP 145:1175
12-13.1	D19S75	11	1	0.09	Brain	CR 54:1397
12-13.1	D19S75	19	3	0.16	Brain	CR 54:1397
13.2	D19S8	21	14	0.67	Brain	AJP 145:1175
Unknown	D19S9	6	2	0.33	Brain	AJP 145:1175
13.3	ERCC1	32	18	0.56	Brain	AJP 145:1175
13.3	ERCC2	16	7	0.44	Brain	AJP 145:1175
13.2	APOC2	25	2	0.08	Breast	GCC 2:191
13.4	D19S22	19	3	0.16	Breast	CR 50:7184
13.2	APOC2	29	3	0.1	Cervix	CR 56:197
Unknown	D19S223	24	3	0.12	Cervix	CR 56:197
Unknown	D19S9	1	0	0	Cervix	CR 49:3598
13.2	APOC2	17	1	0.06	Colon	CCG 48:167
12	D19S7	21	16	0.76	Colon	IJC 53:382
Unknown	D19S210	18	1	0.06	Endocrine	CR 56:599
13.4	D19S22	23	7	0.3	Esophageal	CR 54:2996
Unknown	D19S210	22	7	0.32	Head&Neck	CR 54:1152
Unknown	D19S255	10	0	0	Head&Neck	CR 54:4756
Unknown	D19S255	10	0	0	Head&Neck	CR 54:4756

Chromosome 19 - q Arm

Unknown	D19S210-D19S224	6	0	0	Kidney	PNAS 92:2854
Unknown	D19S210-D19S224	19	0	0	Kidney	PNAS 92:2854
13.4	D19S22	14	3	0.21	Kidney	CR 51:820
Unknown	D19S225	3	0	0	Kidney	PNAS 92:2854
Unknown	D19S225	17	1	0.06	Kidney	PNAS 92:2854
13.4	D19S22	24	11	0.46	Lung	CR 52:2478
13.4	D19S22	3	2	0.67	Lung	CR 52:2478
13.4	D19S22	1	1	1	Lung	CR 52:2478
13.4	D19S22	9	9	1	Lung	CR 52:2478
Unknown	D19S225	22	0	0	Melanoma	CR 56:589
12	D19S7	3	0	0	Neuroblastom a	CR 49:1095
Unknown	CYP1	7	1	0.14	Ovary	CR 50:2724
13.4	D19S22	16	4	0.25	Ovary	CR 51:5318
12-13.1	D19S49	13	3	0.23	Ovary	BJC 69:429
13.2	D19S8	23	5	0.22	Ovary	ICD 54:546
Unknown	D19S8-CYP2A	23	4	0.17	Ovary	CR 53:2393
13.2	D19S8	12	0	0	Prostate	G 11:530
13.4	D19S22	9	3	0.33	Sarcoma	CR 52:2419
12	D19S7	16	1	0.06	Stomach	CR 48:2988
12	D19S7	19	2	0.11	Testis	O 9:2245
13.2	APOC2	11	0	0	Uterus	CR 54:4294
SUM		1066	323	0.3		

Chromosome 20 - p Arm

Band	Marker	Total	Cases with LOH	LOH Frequency	Tumor Type	Reference
12	D20S6	4	1	0.25	Uterus	CR 51:5632
Unknown	Unknown	12	1	0.08	Brain	CR 50:5784
12	D20S6	8	0	0	Brain	CR 49:6572
Unknown	D20S19	6	0	0	Breast	CR 53:3804
Unknown	D20S19	37	2	0.05	Breast	CR 50:7184
12	D20S6	20	3	0.15	Breast	GCC 2:191
Unknown	D20S118	31	0	0	Cervix	CR 56:197
Unknown	D20S19	3	0	0	Cervix	GCC 9:119
12	D20S6	2	0	0	Cervix	CR 49:3598
12	D20S6	28	6	0.21	Cervix	CR 54:4481
Unknown	D20S98	16	2	0.12	Cervix	CR 56:197
Unknown	D20S95	16	0	0	Endocrine	CR 56:599
Unknown	D20S19	59	7	0.12	Esophageal	GCC 10:177
Unknown	D20S72	20	2	0.1	Esophageal	CR 54:2996
Unknown	D20S104	12	0	0	Head&Neck	CR 54:4756
Unknown	D20S104	23	2	0.09	Head&Neck	CR 54:4756
Unknown	D20S95	20	6	0.3	Head&Neck	CR 54:1152
Unknown	D20S104	17	1	0.06	Kidney	PNAS 92:2854
Unknown	D20S104	3	0	0	Kidney	PNAS 92:2854
Unknown	D20S117	5	0	0	Kidney	PNAS 92:2854
Unknown	D20S117	21	0	0	Kidney	PNAS 92:2854
Unknown	D20S19	29	1	0.03	Kidney	CR 51:820
Unknown	D20S19	39	0	0	Liver	CR 51:89
Unknown	D20S19	40	6	0.2	Lung	CR 52:2478
Unknown	D20S104	23	2	0.09	Melanoma	CR 56:589
12	D20S6	2	0	0	Neuroblastom a	CR 49:1095
Unknown	Unknown	16	0	0	Ovary	CR 53:2393
Unknown	D20S19	32	4	0.12	Ovary	CR 51:5118
12	D20S27	14	3	0.21	Ovary	BJC 69:429
12	D20S6	27	4	0.15	Ovary	IJC 54:546
Unknown	D20S19	5	0	0	Pancreas	CR 54:2761
12	D20S5	2	0	0	Pancreas	CR 54:2761
Unknown	D20S5	6	0	0	Prostate	G 11:530
Unknown	D20S19	8	2	0.25	Sarcoma	CR 52:2419
12	D20S5	13	4	0.31	Sarcoma	CR 52:2419
Unknown	D20S19	15	3	0.2	Stomach	CR 52:3099
12	D20S6	22	9	0.41	Testis	O 9:2245
Unknown	D20S19	2	0	0	Uterus	GCC 9:119
12	D20S27	26	0	0	Uterus	CR 54:4294
12	D20S6	4	1	0.25	Uterus	CR 51:5632
90M		684	73	0.11		

Chromosome 20 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
13.3	CSPT1	20	1	0.05	Uterus	CR 54:4294
Unknown	Unknown	20	0	0	Brain	CR 50:5784
13.2	D20S4	15	2	0.13	Breast	GCC 2:191
Unknown	D20S119	26	3	0.12	Cervix	CR 56:197
13.2	D20S4	23	2	0.09	Cervix	CR 54:4481
Unknown	D20S25	25	0	0	Endocrine	CR 56:599
Unknown	D20S19	19	3	0.16	Esophageal	CR 54:2996
Unknown	D20S100	18	1	0.06	Head&Neck	CR 54:4756
Unknown	D20S100	21	2	0.1	Head&Neck	CR 54:4756
Unknown	D20S110	16	1	0.06	Head&Neck	CR 54:1152
Unknown	D20S119	11	1	0.09	Head&Neck	CR 54:1152
Unknown	D20S100	16	0	0	Kidney	PNAS 92:2854
Unknown	D20S100	6	0	0	Kidney	PNAS 92:2854
Unknown	Unknown	5	1	0.2	Liver	BJC 64:1083
13.2	D20S4	15	0	0	Liver	JJCR 81:108
13.2	D20S4	4	0	0	Liver	CCG 48:72
13.2	D20S4	10	1	0.1	Lung	PN 84:9252
13.2	D20S4	10	4	0.4	Lung	PN 86:5099
13.2	D20S4	2	2	1	Lung	PN 86:5099
13.2	D20S4	6	2	0.33	Lung	PN 86:5099
Unknown	D20S100	30	0	0	Melanoma	CR 56:589
Unknown	D20S19	33	0	0	Ovary	IJC 54:546
13.2	D20S4	19	3	0.16	Ovary	CR 53:2393
Unknown	D20S46	14	3	0.21	Ovary	BJC 69:429
Unknown	D20S54	14	1	0.07	Ovary	BJC 69:429
13.2	D20S4	8	0	0	Prostate	G 11:530
13.2	D20S4	11	0	0	Stomach	CR 48:2988
Unknown	D20S19	31	0	0	Testis	O 9:2245
Unknown	D20S26	25	1	0.04	Testis	GCC 13:249
13.2	D20S4	36	4	0.11	Testis	O 9:2245
13.3	CSPT1	20	1	0.05	Uterus	CR 54:4294
SUM		509	38	0.07		

Chromosome 21 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Refer
11.1	D21S52	13	1	0.08	Uterus	CR 51
Unknown	Unknown	14	0	0	Brain	CR 50
22.3	D21S113	5	0	0	Brain	CR 49
Unknown	BCEI	15	2	0.13	Breast	CR 53
Unknown	D21S1	21	1	0.05	Breast	GCC 2
Unknown	D21S112	29	4	0.14	Breast	CR 53
22.3	D21S113	26	4	0.15	Breast	CR 50
22.3	D21S113	3	0	0	Cervix	GCC 9
22.3	D21S113	19	2	0.11	Cervix	CR 54
Unknown	D21S212	26	2	0.08	Cervix	CR 56
Unknown	D21S265	23	0	0	Cervix	CR 56
Unknown	D21S267	14	1	0.07	Cervix	CR 56
Unknown	D21S11	15	0	0	Colon	CGC 4
Unknown	D21S156	16	0	0	Endocrine	CR 56
22.3	D21S113	8	2	0.22	Esophageal	CR 51
22.3	D21S113	30	11	0.37	Esophageal	GCC 1
22.3	D21S113	20	5	0.25	Esophageal	CR 54
Unknown	D21S262	18	0	0	Head&Neck	CR 54
Unknown	D21S262	17	3	0.18	Head&Neck	CR 54
Unknown	D21S59	19	5	0.26	Head&Neck	CR 54
22.3	D21S113	19	3	0.16	Kidney	CR 51
Unknown	D21S262	6	0	0	Kidney	PNAS
Unknown	D21S262	16	0	0	Kidney	PNAS
Unknown	D21S267-D21S265-D21S263	19	1	0.05	Kidney	PNAS
Unknown	D21S267-D21S265-D21S263	6	2	0.33	Kidney	PNAS
22.3	D21S113	15	1	0.07	Liver	CR 51
21.2-TER	D21S19	14	0	0	Liver	CGC
11.1	D21S52	4	1	0.25	Liver	JJCR
22.3	D21S113	28	5	0.18	Lung	CR 52
Unknown	D21S262	23	1	0.04	Melanoma	CR 56
22.3	D21S113	6	0	0	Ovary	O 5:2
22.3	D21S113	12	0	0	Ovary	CR 51
22.3	D21S113	25	2	0.08	Ovary	IJC 5
Unknown	D21S113-11	28	10	0.36	Ovary	CR 53
11.2	D21S120	12	4	0.33	Ovary	BJC 6
22.3	D21S167	13	7	0.54	Ovary	BJC 6
22.3-QTER	D21S171	13	3	0.23	Ovary	BJC 6
22.3	D21S113	3	0	0	Pancreas	CR 54
Unknown	D21S9-D21S17	10	0	0	Prostate	G 11
Unknown	Unknown	6	2	0.33	Sarcoma	CGC 5
22.3	D21S113	15	1	0.07	Sarcoma	CR 52
22.3	D21S113	21	3	0.14	Testis	O 9:2
22.3	D21S113	6	1	0.17	Uterus	GCC 9
22.3	D21S167	20	0	0	Uterus	CR 54
11.1	D21S52	13	1	0.08	Uterus	CR 51

Chromosome 21 - q Arm

SUM	692	90	0.13
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Chromosome 22 - q Arm

Band	Marker	Total	Cases w/LOH	LOH Freq.	Tumor Type	Reference
11.2-13.1	TOPBP2	15	1	0.07	Uterus	CR 54:4294
Unknown	BCR	2	0	0	Brain	CGC 53:271
Unknown	CRYB	7	1	0.14	Brain	CR 50:6783
Unknown	CYP2D	6	4	0.67	Brain	CR 53:2386
Unknown	CYP2D	6	6	1	Brain	CR 53:2386
11.2-12	D22S1	4	0	0	Brain	CR 50:6783
11.2-12	D22S1	7	2	0.29	Brain	CGC 53:271
11.1-11.2	D22S10	5	1	0.2	Brain	CGC 53:271
Unknown	D22S156	4	2	0.5	Brain	CR 53:2386
Unknown	D22S156	4	1	0.25	Brain	CR 53:2386
13.3	D22S171	2	0	0	Brain	CGC 66:117
11.2	D22S20	2	0	0	Brain	CGC 66:117
Unknown	D22S23	8	3	0.38	Brain	CR 50:6783
Unknown	D22S24	1	0	0	Brain	CR 50:6783
Unknown	D22S258	18	2	0.11	Brain	CR 54:1397
Unknown	D22S258	16	1	0.06	Brain	CR 54:1397
Unknown	D22S28	4	3	0.75	Brain	CR 50:6783
Unknown	D22S29	3	2	0.67	Brain	CR 50:6783
Unknown	D22S32	2	0	0	Brain	CGC 66:117
Unknown	D22S32	14	1	0.07	Brain	CR 49:6572
Unknown	D22S32	14	1	0.07	Brain	CR 50:5784
13.1	D22S80	4	0	0	Brain	CGC 66:117
Unknown	D22S9	8	2	0.25	Brain	CGC 53:271
Unknown	D22S9	1	0	0	Brain	CGC 66:117
Unknown	IGLV	2	0	0	Brain	CGC 66:117
Unknown	IGLV	1	0	0	Brain	CR 50:6783
13	IL2RB	18	4	0.22	Brain	CR 54:1397
13	IL2RB	15	0	0	Brain	CR 54:1397
11.1-11.2	LAMBDA1C	4	1	0.25	Brain	CGC 53:271
12.3	MB	5	0	0	Brain	CGC 66:117
12.3	MB	1	1	1	Brain	CGC 53:271
12.3-13.1	PDGFB	1	1	1	Brain	CGC 53:271
11	Unknown	26	10	0.38	Breast	JNCI 84:506
Unknown	D22S10	16	4	0.25	Breast	GCC 2:191
Unknown	D22S113	9	1	0.11	Breast	CR 50:7184
Unknown	D22S9	24	4	0.17	Breast	GCC 2:191
12.3	MB	42	8	0.19	Breast	CR 53:4356
11.1-11.2	D22S10	27	2	0.07	Cervix	CR 54:4481
Unknown	D22S113	8	1	0.12	Cervix	GCC 9:119
Unknown	D22S280	20	3	0.15	Cervix	CR 56:197
Unknown	D22S284	30	4	0.13	Cervix	CR 56:197
11.2-12	D22S1	11	1	0.09	Colon	N 331:273
11.2-12	D22S1	12	4	0.33	Colon	IJC 53:382
11.1-11.2	D22S10	12	0	0	Colon	S 241:961
11.1-11.2	D22S10	13	7	0.54	Colon	IJC 53:382
Unknown	D22S10	29	11	0.38	Colon	CR 50:7166

Chromosome 22 - q Arm

Unknown	D22S9	20	10	0.5	Colon	CR 50:7166
Unknown	D22S9	3	1	0.33	Colon	O 9:991
Unknown	D22S9	17	3	0.18	Colon	N 331:273
Unknown	IGLC	30	15	0.5	Colon	CR 50:7166
Unknown	IGLC	17	3	0.18	Colon	N 331:273
Unknown	IGLC	10	0	0	Colon	S 241:961
Unknown	IGLV	4	0	0	Colon	S 241:961
Unknown	IGLV	27	9	0.33	Colon	CR 50:7166
Unknown	IGLV	30	6	0.2	Colon	N 331:273
12.3-13.1	PDGFB	10	0	0	Colon	S 241:961
Unknown	SIS	4	1	0.25	Colon	N 331:273
Unknown	D22S264	16	0	0	Endocrine	GCC 13:9
Unknown	D22S351	14	1	0.05	Endocrine	CR 56:599
11.2-12	D22S1	21	2	0.1	Esophageal	CR 54:2996
Unknown	D22S32	13	1	0.08	Esophageal	GCC 10:777
Unknown	D22S79	18	3	0.17	Esophageal	CR 51:2113
Unknown	D22S283	25	2	0.08	Head&Neck	CR 54:4756
Unknown	D22S283	22	2	0.09	Head&Neck	CR 54:4756
13	IL2RB	24	7	0.29	Head&Neck	CR 54:1152
Unknown	D22S113	10	2	0.2	Kidney	CR 51:820
12	D22S268	39	1	0.03	Kidney	BJC 69:230
Unknown	D22S280-D22S282	22	0	0	Kidney	PNAS 92:2854
Unknown	D22S280-D22S282	6	0	0	Kidney	PNAS 92:2854
Unknown	D22S283	6	0	0	Kidney	PNAS 92:2854
Unknown	D22S283	16	0	0	Kidney	PNAS 92:2854
11.2-12	D22S1	10	0	0	Liver	JJCR 81:108
Unknown	D22S113	4	0	0	Liver	CR 51:89
Unknown	IGLC	28	9	0.32	Liver	JJCR 84:893
Unknown	IGLC	7	0	0	Liver	CCG 48:72
11.2-12	D22S1	7	2	0.29	Lung	CR 54:5643
11.2-12	D22S1	22	11	0.5	Lung	CR 54:5643
11.2-12	D22S1	3	2	0.67	Lung	CR 54:5643
Unknown	D22S113	16	3	0.19	Lung	CR 52:2478
Unknown	D22S283	35	2	0.06	Melanoma	CR 56:589
11.1-11.2	D22S10	13	3	0.23	Ovary	IJC 54:546
Unknown	D22S113	10	2	0.2	Ovary	CR 51:5118
Unknown	D22S156	10	3	0.3	Ovary	BJC 69:429
Unknown	D22S430-D22S282-D22S283-D22S274	32	23	0.72	Ovary	BJC 70:905
Unknown	D22S9	14	10	0.71	Ovary	CR 53:2393
Unknown	IL-2RB-CYP2D-D22S156	14	4	0.29	Ovary	BJC 72:1330
12.3-13.1	PDGFB	5	1	0.2	Ovary	CR 50:2724
Unknown	SIS	6	0	0	Ovary	CR 49:1220
11.2-13.1	TOPIP2	12	5	0.42	Ovary	BJC 69:429
Unknown	D22S113	4	0	0	Pancreas	CR 54:2761
Unknown	D22S156	26	20	0.77	Pediatric	GCC 15:10

Chromosome 22 - q Arm

Unknown	D22S257	20	10	0.5	Pediatric	GCC 15:10
Unknown	D22S258	23	18	0.78	Pediatric	GCC 15:10
Unknown	D22S264	26	9	0.35	Pediatric	GCC 15:10
Unknown	D22S273	21	14	0.67	Pediatric	GCC 15:10
Unknown	D22S273	26	16	0.62	Pediatric	GCC 15:10
Unknown	D22S274	14	10	0.71	Pediatric	GCC 15:10
Unknown	D22S275	17	13	0.76	Pediatric	GCC 15:10
Unknown	D22S280	25	17	0.68	Pediatric	GCC 15:10
Unknown	D22S281	20	12	0.6	Pediatric	GCC 15:10
Unknown	D22S283	29	18	0.62	Pediatric	GCC 15:10
Unknown	D22S301	20	14	0.7	Pediatric	GCC 15:10
Unknown	D22S303	21	12	0.57	Pediatric	GCC 15:10
Unknown	D22S315	26	18	0.69	Pediatric	GCC 15:10
Unknown	IGLV	10	0	0	Pediatric	CR 50:3279
12.3-13.1	PDGFB	7	1	0.14	Prostate	G 11:530
11.2-12	D22S1	21	8	0.38	Sarcoma	CR 52:2419
Unknown	D22S9	6	2	0.33	Sarcoma	CGC 53:45
11.2-12	D22S1	17	0	0	Stomach	CR 48:2988
Unknown	IGLC	7	2	0.29	Stomach	CR 52:3099
11.1-11.2	D22S10	26	6	0.23	Testis	O 9:2245
12.3-13.1	PDGFB	3	0	0	Testis	CCG 52:72
12.3-13.1	PDGFB	2	0	0	Testis	CCG 52:72
12.3-13.1	PDGFB	1	0	0	Testis	CCG 52:72
Unknown	D22S113	16	3	0.19	Uterus	GCC 9:119
11.2-13.1	TOPIP2	15	1	0.07	Uterus	CR 54:4294
SUM		1594	472	0.3		

Chromosome	Arm	LOH Freq.
1	p	0.26
1	q	0.15
2	p	0.15
2	q	0.12
3	p	0.14
3	q	0.18
4	p	0.13
4	q	0.22
5	p	0.19
5	q	0.27
6	p	0.24
6	q	0.25
7	p	0.12
7	q	0.22
8	p	0.33
8	q	0.14
9	p	0.38
9	q	0.47
10	p	0.18
10	q	0.23
11	p	0.23
11	q	0.26
12	p	0.15
12	q	0.13
13	q	0.29
14	p	0.08
14	q	0.22
15	p	0.11
15	q	0.17
16	p	0.17
16	q	0.36
17	p	0.44
17	q	0.31
18	p	0.12
18	q	0.29
19	p	0.13
19	q	0.3
20	p	0.11
20	q	0.07
21	q	0.13
22	q	0.3

Fig. 5
1) Cyclins

Validation: Deletion of CDC23(Anaphase Promoting), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
9	CDC-25A		1	3p21 U54831
10	CDC-25C		1	5q31 M34065
524	Weel		3	1p15.3-p15.1 X62048
1043	CDC16Hs		2	13 U18291
1278	Cyclin D1		4	11q13 M73554
1280	Cyclin D3		2	6p21 M90814
1298	Cyclin H Assembly Factor		1	4 X87843
1445	Cyclin-Dependent Protein Kinase		2	12 U79269
1450	RAN binding protein 1		1	22 D38076
1523	14-3-3 PROTEIN TAU		1	10 X56468

1) Cyclin dependent kinases/phosphatases

Validation: Deletion of CDC28 (Cyclin Dependent Protein Kinase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1051	CDC28 protein kinase 1		2	17 X54941
1052	CDC28 protein kinase 2		1	9 X54942
1111	Protein phosphatase 1, catalytic subunit, alpha isoform		4	11 M63960
1388	M-PHASE INDUCER PHOSPHATASE 2		1	20 M81934
1401	M-phase phosphoprotein, mpp6		5	7 X98263

1) Cell Division Structural Proteins

Validation: Deletion of CBF2 (Kinetochore Protein), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
20	MCM7 (Minichromosome Maintenance)		3	7q21.3-q22.1 U20980
1246	Chromatin assembly factor-I p60 subunit		2	21 U20980
1273	Chromosome segregation gene homolog CAS		1	20 U33286
1347	High-mobility group (nonhistone chromosomal) protein 1		5	13q12 D63874
1487	Chromatin structural protein homolog (SUPT5H)		3	7 Y12790
1607	Centromere protein B (80kD)		1	20p13 X05299

2) Uniporters

Validation: Deletion of SAT2(Osmotolerance), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1253	ATPase, Ca++ transporting, plasma membrane 2		5	3p26-p25 X63575
1255	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide		4	12p13-qter X03559
1286	Putative Chloride Channel		1	13q14.3-q21.1 X83378
1337	Copper Transport Protein HAH1		1	5 U70660
1407	Nuclear chloride ion channel protein (NCC27)		4	20 U93205
1463	Sodium channel, voltage-gated, type I, beta polypeptide		1	19q13.1 L16242
1505	Transient receptor potential channel 1		1	3 X89066
1521	Voltage-dependent anion channel 2		4	L06328

2) Antiporters

Validation: Proven essential in mammalian cells by tritium suicide selection experiments.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1471	Solute carrier family 9 (sodium/hydrogen exchanger)		1	1p36.1-p35 M81768
1250	ATPase, Na+/K+ transporting, beta 1 polypeptide		1	1q22-q25 X03747
1251	ATPase, Na+/K+ transporting, beta 2 polypeptide		2	17p M81181
1605	Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)		2	7q35-q36 U62531

3) Acyltransferase

Validation: Essential for metabolic processes such as biosynthetic reactions and energy metabolism. The *S. cerevisiae* histone acetyltransferase PAT1 and the N-alpha acetyltransferase which acetylates the N-termini of proteins are essential for growth.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1227	Acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase)		2	3p23-p22 X12966
1387	Lysophosphatidic acid acyltransferase-alpha		7	6 U56417

3) Amino Acid Biogenesis

Validation: Deletion of PRO1(Glutamate 5-Kinase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1330	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)		1	10q24.1-q25.1
1331	Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)		2	16q21
1447	Pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)		1	10q24.3
				X94453

3) Amino Acid Transport

Validation: There are ten essential amino acids in man, which must be transported across the plasma membrane for use in protein synthesis.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1581	Solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1		2	2p16.3
				L11696

3) Addition, removal, or modification of phosphate groups

Validation: Deletion of CMD1(Calmodulin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1269	Calcineurin A catalytic subunit		2	8
1270	Calcineurin B		1	10q21-q22
1351	CALRETICULIN PRECURSOR		1	10q21-q22
1432	SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM		2	10
1476	Snk interacting protein 2-28		1	
				U83236

3) GDP Dissociation Inhibitors

Validation: Deletion of GDI1(GDP dissociation Factor), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1448	RAB GDP DISSOCIATION INHIBITOR ALPHA		2	14q23-q24
				D13988

3) Lactate Transport

Validation: Genes required to maintain organic compounds at levels required for cell growth or survival.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1583	Solute carrier family 16 (monocarboxylic acid transporters), member 1		2	1p13.2-p12 L31801

3) Polyamine Biosynthesis

Validation: Inhibition of polyamine biosynthesis has antiproliferative effects as demonstrated by inhibitors of polyamine metabolism.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1587	Ornithine decarboxylase 1		2	2p25 M16650

3) Protein Glycosylation

Validation: Deletion of DPM1(Dolichol-phosphate mannosyltransferase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1328	Glutamine-fructose-6-phosphate transaminase		1	2p13 M90516
1339	Heparan Heparan Heparan Heparan N-deacetylase/N-sulfotransferase-2		2	10 U36601
1434	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase		3	18 U41514

3) Protein Kinase C

Validation: Deletion of PKC1(Protein Kinase C), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1440	Protein kinase C, beta 1		4	16p11.2 X06318
1443	Protein kinase C-theta		1	10p15 L01087
1444	Protein kinase C substrate 80K-H		1	7 J03075

3) Protein Post-modification

Validation: Deletion of BET2(Geranylgeranyltransferase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1081	geranylgeranyl transferase type II beta-subunit		2	1 X98001

3) Sugar Biosynthesis and Processing

Validation: Deletion of PGI1(Glucose-6-phosphate Isomerase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
14	PIP 5 Kinase beta		2	9q13 X92493
1229	Aconitase 2, mitochondrial		1	22q11.21-q13.3 U80040
1249	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR		2	18 D14710
1257	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1		3	18 X60221
1258	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)		5	21q22.1-q22.2 X83218
1302	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)		5	11 AF001437
1303	Dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)		5	7q31-q32 J03490
1346	Hexokinase 1		3	10q22 M75126
1366	Isocitrate dehydrogenase 2 (NADP ⁺), mitochondrial		2	15q26.1 X69433
1395	NADH dehydrogenase		1	2p16 X81900
1421	NADH:ubiquinone oxidoreductase subunit B13		4	18p11.31-p11.2 U53468
1422	NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8)		1	18p11.31-p11.2 U65579
1424	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR		3	2 X61100
1427	Pyruvate dehydrogenase (lipoamide) beta		9	3p13-q23 M34479
1430	Phosphofructokinase		1	21q22.3 M10036
1451	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KD PROTEIN PRECURSOR		3	1,3 M36647
1464	Succinate dehydrogenase, iron sulphur (Ip) subunit		3	1p22.1-qter D10245
1465	Succinate dehydrogenase 2, flavoprotein (Fp) subunit		10	5p15 D30648
1576	Pyruvate kinase, liver		2	1q21 D10326
1577	Oxoglutarate dehydrogenase (lipoamide)		6	7p14-p13 D10523
1579	Acyl-Coenzyme A dehydrogenase, very		3	17p11.2-p11.13 D43682

	long chain			
1584	Dihydrolipoamide S-succinyltransferase	5	14q24.3	L37418
1588	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	1	1p31	M16827
1590	Pyruvate kinase, muscle	4	15q22	M23725
1596	Phosphoglucomutase 1	5	1p31	M83088
1603	Phosphofructokinase, muscle	4	12q13.3	U24183
1611	Enolase 3, (beta, muscle)	1	17pter-p12	X16504

3) Sugar Transport

Validation: Genes required to maintain organic compounds at levels required for cell growth or survival.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1594	Solute carrier family 2 (facilitated glucose transporter), member 5	3	1p31	M55531
1598	Solute carrier family 5 (sodium/glucose cotransporter), member 2	1	16	M95549

4) Protein Degradation

Validation: Deletion of CDC48(Ubiquitin proteolysis), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1027	26S PROTEASE REGULATORY SUBUNIT 4	3	14	L02426
1037	CALPAIN 1, LARGE	1	11	X04366
1098	Human mRNA for KIAA0123 gene, partial cds	6	9,19	D50913
1114	Proteasome (prosome, macropain) subunit, beta type, 6	7	9,19	D29012
1115	Human mRNA for proteasome subunit z, complete cds	4	9	D38048
1116	PROTEASOME COMPONENT C13 PRECURSOR	2	9	U17496
1117	Human mRNA for proteasome subunit HsC7-I, complete cds	6	1	D26599
1118	Human mRNA for proteasome subunit p112, complete cds	2	2	D44466
1119	Human mRNA for proteasome subunit p27, complete cds	1	2	AB003177
1289	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT	2	19	Z50853

4) Protein Folding

Validation: Deletion of HSP10(Chaperonin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
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1287	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR	1	10	M80254
1305	DNAJ PROTEIN HOMOLOG 2	1	9,2	D13388
1358	DNAJ PROTEIN HOMOLOG HSJ1	2	9,2	X63368

4) Ribosomal Subunit

Validation: Deletion of GRC5(Ribosome), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1127	H.sapiens mRNA for ribosomal protein L11	3	9,2	X79234
1128	Ribosomal protein L17	2	17,4	X52839
1130	60S RIBOSOMAL PROTEIN L18A	5	3	X80822
1131	Ribosomal protein L19	1	17q11	X63527
1133	60S RIBOSOMAL PROTEIN L23A	2	17,18	U43701
1135	Human ribosomal protein L27a mRNA, complete cds	3	6,11	U14968
1136	Human ribosomal protein L28 mRNA, complete cds	11	19	U14969
1137	Ribosomal protein L32	4	20	X03342
1138	Human ribosomal protein L35 mRNA, complete cds	3	20	U12465
1139	Ribosomal protein L35a	1	3q29-qter	X52966
1140	Human mRNA for ribosomal protein L39, complete cds	2	3q29-qter	U57846
1141	Ribosomal protein L4	4	3,6	L20868
1142	Ribosomal protein L6	1	12	X69391
1143	Ribosomal protein L7	1	12	L16558
5	Ribosomal protein L7A	1	19q33-q34	M36072
1144	Ribosomal protein L8	5	12	Z28407
1145	Ribosomal protein L9	2	12	U09953
1146	Ribosomal protein, large, P1	5	15,22	M17886
1147	Human ribosomal protein S10 mRNA, complete cds	1	20	U14972
1148	Ribosomal protein S11	1	19q	X06617
1149	40S RIBOSOMAL PROTEIN S15	2	19q	J02984
1150	40S RIBOSOMAL PROTEIN S15A	2	19q	X84407
1151	Ribosomal protein S16	5	19	M60854
1152	Ribosomal protein S17	5	11pter-p13	M13932
1154	40S RIBOSOMAL PROTEIN S23	2	5	D14530
1155	Ribosomal protein S25	2	11q23.3	M64716
1157	Ribosomal protein S28	2	19	U58682
1158	40S RIBOSOMAL PROTEIN S29	1	19	L31610
1159	Ribosomal protein S5	2	19	U14970
1160	40S RIBOSOMAL PROTEIN S7	3	19	M77233
1161	Ribosomal protein S9	3	19	U14971
1223	Ribosomal protein L7a	6	9q34	X52136

4) T-Complex

Validation: Deletion of CCT2(T-Complex), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1489	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT	1	6	S70154

1490	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT	3	5	D43950
1491	T-COMPLEX PROTEIN 1, GAMMA SUBUNIT	2	1	X74801

4) Translation Elongation

Validation: Deletion of CDC33(eIF4e), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence	
1063	Eukaryotic translation elongation factor 1 delta		3	7	Z21507
1073	Eukaryotic translation initiation factor 4A (eIF-4A) isoform 2		1	18p11.2	D30655
1095	Human mRNA for KIAA0031 gene, complete cds		3	17,2	D21163
1099	Human mRNA for KIAA0219 gene, partial cds		3	12	D86973

4) Translation Factor

Validation: Deletion of CDC33(eIF4e), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence	
1049	PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1		2	12	X81625

4) Translation Initiation Factors

Validation: Deletion of CDC33(eIF4e), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence	
1068	Human translation initiation factor eIF-3 p110 subunit gene		1	16	U46025
1069	EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34		1	17	D21853
1070	Eukaryotic translation initiation factor 4C (eIF-4C)		3	1,X	L18960
1072	Eukaryotic translation initiation factor 2A		2	14	J02645
1074	Eukaryotic translation initiation factor 4E		3	14	M15353
1312	Translation initiation factor 3 (eIF-3) p36 subunit		1	12	U39067

4) tRNA Synthetases

Validation: Deletion of ALA1(Alanyl-tRNA synthetase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1031	Alanyl-tRNA synthetase		2	16q22 D32050
1040	Cysteinyl-tRNA synthetase		1	11p15.5 L06845
1079	Glycyl-tRNA synthetase		2	7p15 U09510
1090	Isoleucine-tRNA synthetase		2	9q21 D28473
1102	ASPARAGINE SYNTHETASE		3	M27396
1121	Arginyl-tRNA synthetase		3	5pter-q11 S80343
1198	Threonyl-tRNA synthetase		1	5p13-cen M63180
1218	VALYL-TRNA SYNTHETASE		4	9 X59303
1221	TRYPTOPHANYL-TRNA SYNTHETASE		1	14 M61715

4) Ubiquitin and Ubiquitin Associated

Validation: Deletion of UFD1(Ubiquitin Fusion), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1309	Ubiquitin carrier protein (E2-EPF)		2	17 M91670
1315	Cyclin-selective ubiquitin carrier protein		2	17 U73379
1362	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 3		2	14 D80012
1363	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T		1	12 X91349
1420	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 14		4	13 M68864
1431	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L1		2	4 X04741
1511	Ubiquitin A-52 residue ribosomal protein fusion product 1		1	19p13.1-p12 S79522
1514	Ubiquitin-conjugating enzyme E2I		6	16p13.3 U45328
1515	Ubiquitin fusion-degradation protein (UFD1L)		4	18 U64444

5) DNA Helicases

Validation: Deletion of DNA2(DNA Helicase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1050	Human CHL1 potential helicase (CHLR1), complete cds		3	18 U33833
1057	ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT		1	2 M30938
1123	RecQ protein-like (DNA helicase Q1-like)		2	12p12-p11 L36140
1397	218kD Mi-2 protein		1	12 X86691

5) DNA Polymerase

Validation: Deletion of POL2(DNA pol epsilon), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1059	Human DNA polymerase delta small subunit mRNA, complete cds		3	12 U21090
1105	DNA polymerase alpha subunit		1	X,11 L24559

5) DNA Replication

Validation: Deletion of CDC45(Chromosomal DNA Replication), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1048	DNA REPLICATION LICENSING FACTOR CDC47 HOMOLOG		1	4 D55716
1094	Human mRNA for KIAA0030 gene, partial cds		2	3 X67334
1124	Replication factor C (activator 1) 1 (145kD)		2	4p14-p13 L14922
1208	DNA topoisomerase I		2	20q12-q13.1 J03250
22	Topoisomerase II		2	17q21-q22 J04088
1222	Minichromosome maintenance deficient (<i>S. cerevisiae</i>) 3		1	17q21-q22 D38073
1461	Replication protein A2 (32kD)		2	1p35 J05249

5) Histone

Validation: Deletion of CSE4(Similar Histone H3), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1335	Histone H1(0)		3	22 X03473
1336	Histone H1x		3	22 D64142
1341	HISTONE H1D		5	6 X57129
1342	HISTONE H2A.1		4	6 U90551
1343	Histone H2A.2		1	6 L19779
1344	Histone H2B.1		1	1 M60756
1345	H4 histone		1	1 X60486

5) Polyadenylation and 3' Cleavage

Validation: Deletion of FIP1(Polyadenylation Factor), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
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1053	Human cleavage and polyadenylation specificity factor mRNA, complete cds	1	11	U37012
1349	HNRNP METHYLTRANSFERASE	4	14	D66904
1426	Poly(A)-binding protein-like 1	2	14	Y00345

5) Purine/Pyrimidine Biosynthesis

Validation: Deletion of CDC8(Thymidylate Kinase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1235	ADENYLOSUCCINATE LYASE	1	1	X65867
1268	CAD PROTEIN	1	2	D78586
1293	CTP synthetase	2	1p34.1	X52142
1326	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	4	21q22.1	X54199
1437	Phosphoribosyl pyrophosphate amidotransferase	2	4q12	U00238
1510	Thymidylate synthase	2	18p11.32	X02308
1517	Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	2	3q13	J03626
1518	Uridine Phosphorylase	1	7	X90858

5) Ribonucleotide Reductase

Validation: Deletion of RNR1(Ribonucleotide Reductase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1452	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN	4	11	X59543

5) RNA Helicase

Validation: Deletion of BRR2(RNA Helicase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1100	Human mRNA for KIAA0224 gene, complete cds	4	16	D86977
1163	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A)	1	1	L13848
1484	PUTATIVE ATP-DEPENDENT RNA HELICASE STE13	3	19	U90426

5) RNA Polymerase II Components

Validation: Deletion of RPA135(RNA pol Subunit), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1026	Homo sapiens (clone mf.18) RNA polymerase II mRNA, complete cds		3	19 L37127
1088	Human RNA polymerase II subunit (hsRFB10) mRNA, complete cds		7	19 U37690
1109	RNA polymerase II, polypeptide C (33kD)		3	16q13-qq21 J05448
1110	Polymerase (RNA) II (DNA directed) polypeptide A (220kD)		1	17p13.1 X63564
1165	DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE		9	17p13.1 J04965
1360	RNA polymerase II subunit hsRFB7		1	11 U20659

5) RNA Polymerase III

Validation: Deletion of RPA135(RNA pol Subunit), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1170	Human RNA polymerase III subunit (RPC62) mRNA, complete cds		1	11 U93867

5) RNA Splicing/Processing

Validation: Deletion of CUS1(U2 snRNP protein), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1171	Human spliceosome associated protein (SAP 145) mRNA, complete cds	0	1	2 U41371
1172	Human splicesomal protein (SAP 61) mRNA, complete cds	3		2 U08815
1176	H.sapiens mRNA for splicing factor SF3a120	1		22 X85237
1177	Splicing factor, arginine/serine-rich 2	2		4,17 M90104
1181	Human splicing factor SRP30c mRNA, complete cds	1		6 U30825
1183	PRE-MRNA SPLICING FACTOR SRP75	2		1 L14076
1216	SPLICING FACTOR U2AF 65 KD SUBUNIT	1		1 X64044
1224	Human (clone E5.1) RNA-binding protein mRNA, complete cds	4		1 L37368
1322	Fibrillarin	1		1 X56597
1354	Heterogeneous nuclear ribonucleoprotein K	1	9q21.32-q21.33	S74678

1455	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A	3	9q21.32-q21.33	X06347
1460	U1 small nuclear RNP-specific C	2	15	X12517
1473	SnRNP core protein Sm D3	2	22	U15009
1474	SnRNP core protein Sm D2	5	22	U15008
1477	U1 snRNP 70K protein	3	19q13.3	M22636
1478	Small nuclear ribonucleoprotein polypeptides B and B1	3	20	J04564
1480	Small nuclear ribonucleoprotein polypeptide N	5	15q12	U41303

5) TATA-Binding Proteins

Validation: Deletion of TAF145(TAFII Complex), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1193	H.sapiens mRNA for transcription factor TFIID subunit TAFII28		1	6 X83928
1196	Human TFIID subunit TAFII55 (TAFII55) mRNA, complete cds		1	5 U18062
1199	TATA box binding protein		2	6q27 M55654
1361	TBP-associated factor (hTAFII130)		1	20 U75308

5) Transcription Elongation Factors

Validation: Deletion of RPO21(RNA pol Subunit), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1077	TRANSCRIPTION ELONGATION FACTOR S-II		4	8 M81601
4	TRANSCRIPTION ELONGATION FACTOR B3		5	5q31 L34587
32	Elongin TCEB1		3	1p36.1 L47345

5) Transcription Factors

Validation: Deletion of BBP1(BFR1p binding), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
33	SUPT6H		3	17q11.2 U46691
1202	Human TFIIA gamma subunit mRNA, complete cds		1	15 U14193
1205	General transcription factor TFIIE beta subunit, 34 kD		1	8p21-p12 X63469
1206	TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT		1	8p21-p12 X16901
1247	CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1		1	19p13.3 X55544
1248	CAMP-dependent transcription factor		3	2 M86842

	ATF-4 (CREB2)			
1274	Transcription Factor (CBFB)	1	2	L20298
1292	CRM1 protein	3	2	Y08614
1368	Transcription Factor IL-4 Stat	1	21q21-q22.1	U16031
1373	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	1	21q21-q22.1	M97935
1411	Nuclear Factor I-B2 (NFIB2)	1	19	U85193
1483	Transcription Factor Stat5b	1	17	U48730
1496	Transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	2	15q21	M83233
1497	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	8	19p13.3	M31523
1498	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	1	7p	M62810
1500	TRANSCRIPTION FACTOR P65	3	11	L19067
1501	Transcription factor COUP 2 (a.k.a. ARF1)	2	15q26.1-q26.2	X91504

6) Clathrin

Validation: Deletion of RET1(Alpha-Cop), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1242	CLATHRIN COAT ASSEMBLY PROTEIN AP47	2	8	D38293
1243	CLATHRIN COAT ASSEMBLY PROTEIN AP50	6	3	U36188
1282	cell surface protein	5	22	X83545
1290	Clathrin, light polypeptide (Lcb)	1	4q2-q3	M20470
1291	Clathrin heavy chain	4	17q11-qter	U41763

6) Cytoskeleton

Validation: Deletion of MHP1(Microtubule Interacting), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1	Actin, gamma Subunit Sh3p17(Myosin IC Heavy Chain)	8	17p11-qter	X04098
1032	Actin depolymerizing factor [human, fetal brain, mRNA, 1452 nt]	4	1 21	U61166
1038	Capping protein (actin filament), gelsolin-like	3	2cen-q24	M94345
1039	Human capping protein alpha mRNA, partial cds	2	7	U03851
1056	Desmin	1	2q35	J03191
1080	Gelsolin (amyloidosis, Finnish type)	1	9q34	X04412
1092	Keratin 19	5		Y00503
1093	KERATIN, TYPE II CYTOSKELETAL 6D	13	5,12	J00269
1267	BETA-CENTRACTIN	1	2	X82207
1284	Cofilin 1 (non-muscle)	5	11q13	X95404
1383	LAMIN A	1	20	M13451
1385	Lamin B receptor	1	1q42.1	L25931

1386	MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM	1	12,17	M22920
1404	MYOSIN HEAVY CHAIN 95F	1	4p16.3	U90236
1405	MYOSIN HEAVY CHAIN IB	1	13	D63476
1406	Myosin-IC	1	13	U14391
1486	SUPPRESSOR OF TUBULIN STU2	1	11	X92474
1495	MICROTUBULE-ASSOCIATED PROTEIN TAU	1	17	J03778
1507	Tubulin, gamma polypeptide	1	17	M61764
1508	TUBULIN ALPHA-4 CHAIN	1	17	X06956
1520	Myosin VIIA (USH1B)	2	17	U39226

6) ER Protein

Validation: Deletion of BET1(v-SNARE), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1272	Calnexin	1	5q35	M94859
1317	ER LUMEN PROTEIN RETAINING RECEPTOR 2	1	19	M88458
1614	Ribophorin I	4	3q	Y00281
1615	Ribophorin II	1	20q12-q13.1	Y00282

6) Integrin

Validation: Deletion of MYO2(Myosin Heavy Chain), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1378	Integrin alpha-3 subunit	1	5q23-q31	M59911

6) Karyopherin

Validation: Deletion of KAP121(Karyopherin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1091	karyopherin alpha 3	3	13	D89618
1214	transportin (TRN)	1	13	U70322

6) Lysosomal Proteins

Validation: Essential for sequestering and degrading aged or defective organelles and polymers that can interfere with cell survival, proliferation as seen by human diseases such as Tay-Sachs disease.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1265	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD		2	22pter-q11.2 X76228

6) MITOCHONDRIAL IMPORT

Validation: Genes required to maintain inorganic ions at levels compatible with cell growth or survival.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1578	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20		8	1 D13641

6) Nuclear Pore Complex

Validation: Deletion of GSP1(Nuclear Pore Trafficking), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
28	Nuclear Pore Complex NUP214		3	9 D14689
29	Nucleoporin 98		3	11p15 U41815
1266	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C		4	20 L38696
1350	Heterogeneous nuclear ribonucleoprotein A1		4	12q13.1 X79536
1355	Nuclear pore complex protein hnup153		3	6 Z25535
1425	NUCLEAR PORE GLYCOPROTEIN P62		1	11 X58521
1449	Export protein Rae1		5	20 U84720
1454	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2		3	12 M29063
1524	140 KD NUCLEOLAR PHOSPHOPROTEIN		5	10 D21262

6) Protein Transport

Validation: Deletion of BET3(v-SNARE associated), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
8	Integral Transmembrane Protein		3	11q23-24 L38961
1467	Sec23A isoform		2	14 X97064
1608	Signal recognition particle receptor (('docking protein'))		8	11q23-q24 X06272
1613	TIM17 preprotein translocase		2	1 X97544

6) Syntaxin

Validation: Deletion of SED5(Syntaxin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1186	syntaxin 1A		1	21q22.1
1188	syntaxin 3		1	11
1189	Syntaxin 5A		2	11
1190	syntaxin 7		1	6

6) Vacuolar Protein

Validation: Deletion of PPA1(Vacuolar H-ATPase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1261	Vacuolar H+ ATPase proton channel subunit		2	6

6) Vesicle Proteins

Validation: Deletion of SAR1(COP II), a *S. cerevisiae* gene in the same biochemical family, is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1025	Human (chromosome 3p25) membrane protein mRNA		3	3,18
24	COATOMER BETA SUBUNIT		1	3
1055	COATOMER DELTA SUBUNIT		8	11
1082	Human GP36b glycoprotein mRNA, complete cds		3	5
1173	SEC14 (<i>S. cerevisiae</i>)-like		7	17q25.1-q25.2
1174	Human homologue of yeast sec7 mRNA, complete cds		2	17q25.1-q25.2
1184	Human chromosome 17q21 mRNA clone LF113		1	17
1217	H.sapiens mRNA for vacuolar-type H(+)-ATPase 115 kDa subunit		2	17

99) Direct Essential Yeast Homolog

Validation: Deletion of the *S. cerevisiae* homologue of this gene is lethal.

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1238	Aldolase A		2	16q22-q24
1239	Aldolase B, fructose-bisphosphate		2	9q22
1241	S-adenosylmethionine decarboxylase 1		1	6q21-q22
1271	Calmodulin 1 (phosphorylase kinase, delta)		1	14q24-q31
1300	DED81		1	18

1301	Deoxyhypusine synthase	3	19p13.11-p13.12	L39068
1306	Dolichol monophosphate mannose synthase (DPM1)	2	20	AF007875
1318	ESS1 PROTEIN	1	19	U49070
1332	Glucose phosphate isomerase	1	19q13.1	K03515
1333	Guanylate kinase (GUK1)	3	19q13.1	L76200
1359	Heat shock 60 kD protein 1 (chaperonin)	1	9	M34664
1367	PERIODIC TRYPTOPHAN PROTEIN 1	1	12	L07758
1372	IPP isomerase	1	10	X17025
1396	N-acetylglucosaminyltransferase I	4	5q31.2-q31.3	M55621
1399	Mannose phosphate isomerase	3	15q22-qter	X76057
1414	Nipl	1	5	U15172
1415	GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE	2	17	M86707
1433	PHOSPHATIDYLINOSITOL 4-KINASE ALPHA	10	17	L36151
1446	PERIODIC TRYPTOPHAN PROTEIN 2	2	8	U53346
1519	Uridine diphosphoglucose pyrophosphorylase	1	2	U27460

Fig. 6

Target Variances by Field Table for Conditionally Essential Genes

Conditionally Essential Biosynthetic Enzymes

Validation: Conditionally Essential

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1536	5-methyltetrahydrofolate-homocysteine methyltransferase		3	U75743
1539	Glutamate-ammonia ligase (glutamine synthase)		5	1q31 X59834

Proteins that Repair Radiation Induced DNA Damage

Validation: Conditionally Essential

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1541	Fanconi anemia complementation group C		1	9q22.3 X66894

Proteins of DNA Repair

Validation: Conditionally Essential

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1528	DNA excision repair protein ERCC5		4	13q33 D16305
1530	HHR23A protein		3	9 D21235
1532	DNA EXCISION REPAIR PROTEIN ERCC-1		2	19q13.2-q13.3 M13194
1533	DNA repair helicase ERCC3		1	2q21 M31899
1537	URACIL-DNA GLYCOSYLASE 1 PRECURSOR		2	8 X15653
1526	Damage-specific DNA binding protein 1 (127 kD)		2	11, 15 AJ002955

Proteins that repair chemically induced DNA damage

Validation: Conditionally Essential

ID	Name	Variances Identified	Chromosome	Genbank Sequence
1534	O-6-methylguanine-DNA methyltransferase		4	10q26 M60761

Fig. 7

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1.01	472	CGGCCATGTA [C/T] GTGGCCATCC	71 (36)	1 (1)	Silent
.02	250	ACGAGGCCCA [G/A] AGCAAGCGTG	71 (36)	1 (1)	Silent
.03	1003	CGGGCATTGC [C/T] GACAGGATGC	66 (35)	6 (5)	Silent
.04	801	ACGAGCTGCC [C/T] GATGGCCAGG	71 (36)	1 (1)	Silent
.05	1201	AATGCTTCTA [A/G] ACGGACTCAG	71 (36)	1 (1)	Silent
.06	991	CCACCATGTA [C/T] CCGGGCATTG	17 (17)	56 (35)	Silent
.07	1099	TGTGGATCGG [T/C] GGCTCCATCC	71 (36)	1 (1)	Silent
.08	499	GTGCTGTCCCT [C/G] TACGCCTCT	65 (65)	7 (7)	Silent
4.01	2168	CCGCCAGTAG [C/T] ATCAGCTTTA	61 (34)	11 (9)	3'UT
.02	388	TGGAAGCCA [C/T] GGGAGCCGA	62 (29)	10 (7)	Thr->Met
.03	491	AGAGGAGAGA [T/C] GAGAGAAAGA	68 (36)	4 (4)	Silent
.04	1171	AAAACTAATT [T/C] GGATAGAAAG	68 (36)	4 (4)	Leu->Ala
.05	336	TCGGGATGCC [C/T] TGCAGAAGGA	71 (36)	1 (1)	Silent
5.01	421	ACGTCCCAAC [G/A] AAGAGACCAC	66 (36)	6 (6)	Silent
8.01	1570	CTCCGTCCA [T/C] TGTACTATCTG	70 (36)	2 (2)	Silent
.02	778	TCCACGTCTT [C/G] GTGCTGATGC	71 (36)	1 (1)	Silent
.03	158	GGACACACTT [T/C] TGAAGCTTCT	71 (36)	1 (1)	Silent
9.01	1929	CCATGCACCA [C/A] GAGGACTTTA	71 (36)	1 (1)	His->Gln
10.01	1099	AACCGTGT CAGGGAAACACCA	69 (36)	3 (3)	Gly->Arg
14.01	911	CAATTCAATC [G/A] CCGCCCTAAA	69 (36)	3 (3)	Arg->His
.02	1174	CAACAGTAA [G/A] TGAAAATGGT	71 (36)	1 (1)	
20.01	1627	CCCAGCACAT [C/T] ACCTATGTGC	44 (30)	28 (21)	Silent
.02	2041	GCCGAAGTGT [C/G] CGGTTCTCTG	71 (36)	1 (1)	Asp->Glu
.03	1393	cagccatcca [c/t] gaggtcatgg	71 (36)	1 (1)	Silent
22.01	4008	CAACAAAAAC [A/C] AAATTCACAA	71 (36)	1 (1)	Silent
.02	4446	AGCCATCCAC [T/G] TCTGATGATT	71 (36)	1 (1)	Silent
24.01	1101	GCCACTGGCA [G/A] TAAAGGATAT	71 (36)	1 (1)	Val->Ile
28.01	5009	TGCCACGCCC [G/C] TGTTTGGGCA	70 (36)	2 (2)	Val->Leu
.02	2023	AGAAATCACC [C/T] AGGATAACCC	71 (36)	1 (1)	Silent
.03	2041	CCCCTCCAGC [G/A] GCAAAGCCAG	71 (36)	1 (1)	Silent
29.01	1768	CCCTGCCACT [A/C] GAGTCCGGCC	67 (36)	5 (5)	Silent
.02	2781	AGGAGCATCC [G/A] TCTAAAACTA	70 (36)	2 (2)	Silent
.03		2 bp deletion			3'UT
32.01	1171	AAAACTAATT [T/C] GGATAGAAAG	70 (36)	2 (2)	Leu->Ala
.02	388	TGGAAGCCA [C/T] GGGAGCCGA	59 (33)	13 (10)	Pro->Met
.03	2168	CGGCCAGTAGCATCAGCTTTA	60 (34)	12 (10)	Silent
33.01	2397	GGCTAGATGG [T/C] CTGGCCAAAA	47 (33)	25 (12)	Silent
.02	3708	AGGTGCGGGT [C/T] GATGTCAACC	63 (35)	9 (8)	Silent
.03	3795	GGACCCACCT [C/A] CTGAAGATCC	62 (35)	10 (9)	Silent
524.01	1598	CACAAGTTGA [G/A] GAGGGCGATA	68 (36)	4 (4)	Silent
.02	2548	CTTATATTTC [T] ¹⁰ GATGTCAACC	71 (36)	1 (1)	3'UT
.03	3158	AAAATTGTCT [GTTT] GTTTTCTCAT	50 (34)	22 (20)	3'UT
525.01	255	CTGCGGTTCT [C/T] GAGGGCGATA	54 (34)	18 (16)	Silent
.02	346	CGTGCGGGCT [C/T] TTCACCATCC	71 (36)	1 (1)	Leu->Phe
.03	523	CCCCATCCTC [A/G] TCCCGTGCCA	63 (36)	9 (9)	Ile->Val
1025.01	1051	CAACTAACCA [G/A] ACAACTGGGA	24 (20)	48 (44)	3'UT

.11	418	CCCCCTTTTG [C/T] AGCCCAAGGC	6 (5)	5 (3)	N/D
.12	640	CAACTAACCA [G/A] ACAACTGGGA	15 (7)	7 (6)	N/D
1026.2	47	GTCTGGACGC [G/A] ACGGCGGCGG	2 (2)	3 (2)	5' UT
.9	262	CCCACCCCTT [G/A] GAGACAAGA	28 (13)	4 (1)	Silent
.19	602	ATAAAGTATAGCGG [A/G] AGAGAN	5 (5)	11 (8)	3' UT
1027.2	405	TGGAAGAGAT [T/C] ATTGATGACA	2 (2)	2 (2)	Silent
.6	942	GGACAAAAAG [A/G] TATGACTCCA	8 (8)	4 (4)	Silent
.16	1361	CAGGAAGGCA [C/A] CCTTGAGGGG	13 (11)	3 (3)	Thr -> Asn
1031.31	2990	CCTTCGCCCA [G/A] CTGCGCTCG	9 (7)	2 (2)	Silent
.32	2991	CTTCGCCAG [C/G] TCGCCTCGG	4 (4)	4 (4)	Leu -> Val
1032.1	3	AGTCGCCG [G/A] GGAGGACGGTCT	5 (4)	3 (3)	5' UT
.2	4	GTCCCG [G/A] GAGGACGGTCTGC	5 (5)	3 (2)	5' UT
.3	69	CCGCCGCGGC [G/A] AAGATGGCCT	5 (5)	2 (2)	5' UT
.10	312	AAAAGATTG [T/C] CGCTATGCTT	8 (8)	3 (3)	Silent
1037.20	2919	TGGTTATGGG [G/C] GTGCCAGAGG	15 (13)	2 (2)	3' UT
1038.5	723	CAGGTCCTGG [G/C] CCCAAGCCT	7 (7)	3 (3)	Silent
.10	862	ACTCCAGCCC [C/A] TTTGCCCTTG	5 (5)	13 (10)	Silent
.13	1053	CCTCAGGGCC [G/A] TGAGAGTCCC	13 (10)	8 (7)	Arg -> His
1039.19	1665	ACCATGTCTC [A/G] GTTTATTTT	2 (2)	6 (5)	3' UT
.23	1748	TATTTAGTA [G/A] AAAATCACTT	3 (3)	2 (2)	3' UT
1040.7	2056	GCTGAAGAAG [T/C] CTTCGAGGCT	20 (16)	2 (2)	3' UT
1043.1	351	ACTTGAAGGA [T/C] GAAAGTGGCT	2 (2)	3 (3)	Silent
.2	372	TCAAAGATCC [C/T] TCCAGCGACT	2 (2)	3 (3)	Silent
1048.3	341	GCTACGCGAA [G/A] CTCTTGCTG	2 (2)	2 (2)	Silent
1049.10	2648	CCTGAAACCC [T/A] GAAGCTGATG	5 (4)	3 (1)	3' UT
.12	2768	CAGTGGTAGC [G/A] ATGGAAGAAA	8 (6)	2 (1)	3' UT
1050.11	2381	CAGGAAGAAG [A/G] TATTCAGGA	4 (2)	2 (2)	Ile -> Val
.13	2750	TTTGGCCAGC [G/A] TAGTGCTCCT	2 (2)	2 (1)	Val -> Ile
.14	3034	GAGTCCAGAG [T/C] GCTGCCAGGA	2 (2)	2 (1)	3' UT
1051.10	260	AGCTGGCAAG [C/T] TACTTTTCAG	15 (10)	3 (1)	3' UT
.18	409	TTTGCTTCTT [G/A] AGTAGAGCCA	17 (12)	3 (1)	3' UT
1052.7	428	TGTACAAATC [T/C] TTCATCCATA	7 (6)	2 (2)	3' UT
1053.24	4113	AGGAGAAGAC [C/T] TACCGGCGGC	8 (7)	8 (8)	Silent
1055.17	3122	CAGCGTCAGC [C/A] AGCTCAGCCT	4 (4)	4 (4)	3' UT
.23	3450	TGAGAAGGGC [T/C] TGGACAAGA	26 (12)	3 (3)	3' UT
.25	3568	TCAAAAACC [T/C] TTTTCTG	26 (12)	2 (2)	3' UT
.01	2061	AGGCTGGTCG [C/T] GAACTCCTGA	61 (34)	11 (9)	3' UT
.02	2419	TTAAAGATA [C/A] GCATGTCTTC	59 (33)	13 (10)	3' UT
.03	3047	TAAGTCTTT [G/T] AGTGTCTATCA	71 (36)	1 (1)	3' UT
.04	2960	TATTACTCAC [G/A] TATACCCAT	71 (36)	1 (1)	3' UT
.05	3450	TGAGAAGGGC [T/C] TGGACAAGA	60 (33)	12 (9)	3' UT
.06	3296	CTGCAAGAG [T/C] GTACTGTGCT	60 (33)	12 (9)	3' UT
1056.12	407	CAAGAGCACC [G/C] GTGGGCCCC	13 (9)	2 (2)	Val -> Arg
1057.20	3067	TAACTTTTCG [G/A] TCTTTCCCAT	7 (5)	3 (3)	3' UT
1059.11	1130	AACGTGAGTG [A/G] CATTTTCCGA	5 (5)	2 (2)	Asp -> Ala

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.19	1327	AATCATCCGA (G/A) GTCCTGAGGA	19 (14)	3 (3)	Val -> Ser
.27	1474	GGGAGGCCCTG (G/A) GGCTGGGCC	15 (11)	2 (2)	Gly -> Arg
1063.21	705	CGGACATGGC (C/T) CAGCTGGAGG	8 (7)	8 (7)	Silent
.22	721	GGAGGCCCTGT (G/T) TGCCTCTAT	16 (14)	2 (2)	Val -> Leu
.38	949	GCGTGCGTGA (G/A) GGCCCTGCCA	2 (2)	2 (2)	3' UT
1068.30	2756	GCGCCGCGGT (G/C) GCTACGCCA	21 (15)	2 (2)	Ala -> Arg
1069.10	1199	GGGCGCCAGC (C/G) GAGTGCTTAT	17 (13)	2 (2)	Arg -> Glu
1070.3	303	AAGAGGATGG (G/T) CAGGAGTATG	3 (2)	6 (6)	Gly -> Val
.7	615	ACATTGGAGA (T/C) GATGATGAAG	6 (6)	2 (1)	Silent
.12	1092	GAAGTCTGCA (G/T) TTGAAGAAAA	5 (5)	3 (3)	3' UT
1072.20	1309	TCACGAGATT (T/C) GCCAGGGGCA	15 (10)	2 (2)	3' UT
.21	1310	CACGAGATTT (G/T) CCAGGGGCAT	4 (3)	5 (5)	3' UT
1073.2	65	GGCCCAGAGG (G/A) AATGGACCCC	2 (1)	2 (2)	Silent
1074.18	1428	TTGTGTGATT (T/C) CCTAAACATA	5 (4)	2 (2)	3' UT
.21	1650	TTGTCTTTTA (G/A) ACAACTAGAT	6 (6)	3 (3)	3' UT
.22	1652	GTCTTTTAGA (C/A) AACTAGATTT	5 (5)	3 (3)	3' UT
1077.19	1275	TATAATAATT (G/T) TATGGTACCT	3 (2)	3 (3)	3' UT
.22	1585	ATGTACATAA (T/A) TTTGAGGTAG	7 (5)	3 (1)	3' UT
.30	2336	TCAGGCACCC (A/G) TAGAAAGACC	4 (3)	10 (9)	3' UT
.34	2460	GAATTGGCCC (G/A) CTGGTACCAA	5 (4)	16 (14)	3' UT
1079.11	2035	CTGCTGTAGT (T/C) GCTCCATTCA	19 (14)	2 (1)	Silent
.18	2347	GCAACATCAC (A/G) TGGGCTGATG	25 (17)	2 (2)	Silent
1080.24	2367	TGCCTGAGGA (A/C) GGGCAGGGCC	1 (1)	5 (4)	3' UT
1081.17	805	GATTGATAGA (G/A) AGAAACTGCG	13 (8)	2 (1)	Ser -> Lys
.36	1178	ATGCATATTGTAAATAAA (A/G) A	2 (2)	10 (9)	3' UT
1082.19	767	TTGGGGGCTT (C/T) CGCCGGCACC	7 (5)	2 (2)	Ser -> Phe
.27	924	ACGTGGACGA (C/A) CCCACGGGGA	3 (3)	3 (3)	Asp -> Glu
.40	1333	GTCTACAGAT (G/T) GGCTGTGGCC	4 (4)	5 (5)	3' UT
1088.11	112	CCGAGGGGGA (C/T) GCGCTGGATG	23 (16)	7 (5)	Silent
.12	144	AAGCGCTACT (G/C) CTGCCGCCGG	24 (18)	5 (4)	Cys -> Ser
.13	145	AGCGCTACTG (C/G) TGCGCGCGGA	21 (16)	5 (4)	Cys -> Trp
.20	226	GACCACGCTG (A/G) AACCCACCCA	23 (16)	18 (11)	3' UT
.21	238	ACCCACCCAC (C/A) CGCTGTGCTG	31 (19)	3 (3)	3' UT
.24	270	TGAGCGTCTT (A/G) CCCCGAATTC	29 (18)	9 (6)	3' UT
.27	338	GTGTGTATCC (C/G) ATACCCCACT	23 (15)	2 (2)	3' UT
1090.18	4153	GTGTAAAATA (T/C) GCTGCTTGGA	13 (12)	2 (2)	3' UT
.21	4215	CTCACAGTAA (T/C) CTTCACTT	21 (16)	2 (1)	3' UT
1091.3	793	AGGATCCCCC (A/G) CCGCCTATGG	2 (1)	5 (2)	Silent
.9	962	CTTTCTTGTG (C/T) CCCTTCTGAG	4 (3)	5 (2)	Pro -> Ser
.14	2078	AAGAGGTGCA (A/G) TGTGATCTGA	6 (5)	11 (8)	3' UT
1092.5	342	CCTGGAGGCG (G/C) CCAACGGCGA	16 (8)	4 (1)	Ala -> Pro
.10	401	GGCCTGGGCC (C/T) TCCCGCGACT	9 (6)	11 (5)	Silent
.11	503	AGATCGACAA (C/T) GCCCGTCTGG	11 (6)	6 (5)	Silent
.22	1034	TTGGAGCCCA (G/C) CTGGCGCATA	4 (4)	3 (2)	Gln -> His

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.23	1035	TGGAGCCAG [C/G] TGGCGCATAT	3 (3)	3 (2)	Leu -> Val
1093.2	258	CTCTCACAGA [C/T] GAGATCAACT	3 (2)	2 (1)	Silent
.3	330	CAGACACATC [T/C] GTGGTGCTGT	3 (2)	3 (2)	Silent
.4	339	CTGTGGTGCT [G/A] TCCATGGACA	3 (2)	3 (2)	Silent
.6	420	TTGCTCAGAG [A/G] AGCCGGGCTG	3 (2)	3 (2)	Silent
.22	954	GCGTTGGAGG [T/C] GGCTTCAGTT	7 (2)	3 (1)	Val -> Ala
.23	960	GAGGTGGCTT [C/T] AGTTCAGCA	7 (2)	3 (1)	Silent
.24	972	GTTCCAGCAG [T/C] GGCAGAGCCA	7 (2)	3 (1)	Silent
.27	983	GGCAGAGCCA [T/C] TGGGGGTGGC	7 (2)	3 (1)	Ile -> Thr
.28	1065	GGAAGAGCTA [T/C] AAGCACTAAA	9 (3)	3 (1)	Silent
.44	1198	TAGAGCTGGG [G/T] ATGAATGCTT	13 (2)	3 (1)	3' UT
.45	1202	GCTGGGGATG [A/G] ATGCTTAGTG	13 (2)	4 (1)	3' UT
.49	1579	TGTGCTCTTC [A/G] CTCTTTGCAA	14 (3)	5 (2)	3' UT
.50	1582	GCTCTTCACT [C/G] TTTGCAATTG	13 (3)	6 (3)	3' UT
1094.24	3103	TGCTTTTGCT [C/G] GCTTTGGCCA	15 (9)	4 (2)	3' UT
.25	3104	GCTTTTGCTC [G/C] CTTTGGCCAG	2 (2)	4 (2)	3' UT
1095.17	2885	CGTAGGAAGG [G/C] CCTCAGTGAA	18 (11)	2 (2)	Silent
.25	2994	GTGGACTCCT [G/T] GGAGCTCCTG	14 (10)	3 (3)	3' UT
.31	3246	GGGGATGAAA [C/A] CCCAAGGGGC	10 (7)	12 (11)	3' UT
1098.10	1486	GGCAGTGGCC [G/C] CCTGGGTGA	8 (7)	3 (3)	Ala -> Pro
.13	1522	CACGTATGAG [G/C] ACATCCAGAC	2 (1)	12 (10)	Asp -> His
.21	1740	TGCATTCTTT [T/C] GGAACCAAT	11 (6)	2 (2)	3' UT
.25	1850	GGAGGGCGGT [C/T] GGTGCTTCCC	21 (13)	2 (2)	3' UT
.29	1942	TGACCTATCA [A/G] AGCCTCCCGG	16 (11)	6 (5)	3' UT
.35	2029	CCAAGGAGCG [C/A] GCTCCACGCG	13 (10)	2 (2)	3' UT
1099.36	7590	TGGTTTGAGA [G/C] CTGGCGCTAC	12 (11)	6 (4)	3' UT
.37	7591	GGTTTGAGAG [C/G] TGGCGCTACC	9 (8)	6 (4)	3' UT
.44	7705	ATGGATCTGA [C/T] CCCTGTCAGA	13 (12)	9 (8)	3' UT
.01	215	ATTCTCTAGT [C/T] CTTTCATGATG	63 (36)	9 (9)	Ile->Val
.02		Nucleotide repeat	66 (35)	6 (5)	3' UT
1100.16	3865	ATTGGGTCTCT [C/G] AGCCTTCTGG	4 (3)	4 (3)	3' UT
.17	3904	GGACAAAGCC [T/C] TTTCATCTGA	2 (2)	4 (3)	3' UT
.19	3994	GGTGGAGTTC [T/C] TCCATGCAGG	6 (6)	6 (5)	3' UT
.22	4046	TATCCGAGGT [G/T] CTGCCGGGGC	6 (6)	5 (5)	3' UT
1102.29	1967	TAAGTTGGGT [T/G] TGAAAAAAT	2 (1)	25 (20)	3' UT
.30	1982	AAAAATAAAA [T/G] TCCTAAATTT	2 (1)	24 (20)	3' UT
.31	1991	AAAAATAAAATTCCTAAAT [T/C] T	2 (1)	21 (17)	3' UT
1105.15	2038	GGGCCTGCCT [G/C] TGAGTGGTGC	3 (3)	6 (6)	3' UT
1109.4	884	AGCTTGCCCTG [C/T] TTCAGCAAAA	4 (4)	2 (1)	3' UT
1110.11	6466	CTGATGCAGA [T/C] TCTTGCTTGT	5 (5)	5 (5)	3' UT
1111.8	794	AAGACGGCTA [T/C] GAGTTCTTTG	2 (1)	7 (6)	Silent
.15	1087	CTGCCATGCT [G/T] GGGGGGGGTC	8 (5)	4 (4)	3' UT
.16	1110	CCCGACCCCT [A/C] AGGCCACCT	3 (1)	18 (17)	3' UT
.17	1146	GAGCCTTGGT [G/T] TATTTTCTT	22 (18)	4 (4)	3' UT
1114.18	540	ATGCTACCTA [C/T] CGGGAAGGCA	29 (16)	2 (2)	Silent
.20	585	TCAGTGCCAA [T/A] GCTCTCGCTT	22 (15)	6 (4)	Asn -> Lys
.21	586	CACGCGCAAT [G/T] CTCTCGCTTT	16 (12)	6 (4)	Ala -> Ser
.27	704	CCCAAAATCG [C/T] CGTTGCCACT	20 (14)	3 (3)	Ala -> Val
.01	177	GAACAACCAC [T/C] GGGTCCTACA	70 (36)	2 (2)	Silent
.02	328	ACTGAATGAG [C/G] CTCCACTGGT	71 (36)	1 (1)	Pro->Ala

.03	328	GGCCGGAGGC (A/G) TTCACTCCAG	30 (20)	42 (32)	Silent
1115.2	77	ACTGCCGCAG (G/A) AATGCCGTCT	13 (9)	4 (1)	Silent

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.5	130	CTTCCAAAGG [T/C] CCGGAAAAGT	8 (7)	14 (4)	Val -> Ala
.15	643	TTCAACGACC [T/C] GGGCTCCGGA	11 (8)	2 (1)	Leu -> Pro
.16	732	CAAGAAGGGG [A/C] CCAGGCTTGG	12 (7)	4 (2)	Thr -> Pro
1116.2	121	CGGACCGTCC [T/A] GACTACAGTT	2 (1)	4 (4)	Silent
.3	173	CCGGGGAATG [A/C] AGCCACAGA	2 (1)	5 (5)	Lys -> Gln
1117.1	15	CCTGCAGCCC [T/C] GGCCTTCCGC	10 (7)	4 (3)	5' UT
.2	16	CTGCAGCCCT [G/T] GCCTTCCGCC	10 (7)	4 (3)	5' UT
.5	19	CAGCCCTGGC [C/T] TTCCGCCACC	10 (7)	2 (2)	5' UT
.19	401	TGGCAGCCTT [G/T] GCCAAGGCCC	12 (7)	8 (4)	Leu -> Phe
.01	1287	GCCATGCACT [C/G] ACCAACGCCA	65 (36)	7 (7)	Ser->Val
.02	3385	TTGCCTGGAC [G/A] TTGCCTGCG	70 (36)	2 (2)	3' UT
1118.5	1681	GACATGGTTG [G/A] TTATGCACAA	6 (5)	2 (1)	Val -> Asp
.28	2945	ATGATTAAAG [A/G] CCAGAGGATC	7 (6)	7 (5)	3' UT
1119.11	1075	TCACAAATTA [G/A] GCCACGGCCC	3 (3)	3 (3)	3' UT
1121.17	1524	CATCCGTTGC [A/G] TATGGCTGCA	3 (3)	2 (2)	Silent
.23	1669	TGCACGTCCT [G/C] CCAATATTGA	6 (6)	3 (3)	Ala -> Pro
.27	1902	GACGACTGG [G/A] AAAATATTGA	2 (2)	20 (17)	Gly -> Glu
1123.9	2485	CCTGATATGA [A/C] TGTACTAAA	5 (5)	4 (4)	Asn -> Thr
.17	2807	TTGACATAAC [T/C] ATCTTTTGA	4 (3)	3 (3)	3' UT
1124.2	119	TCTTATCGGA [G/A] CTTGTATGTG	2 (1)	3 (3)	5' UT
.7	3616	TACTCCATAC [G/T] CACTTCAAGC	2 (1)	5 (3)	Ala -> Ser
1127.2	4	TGCAAAA [G/A] CGCAGGATCAAGG	13 (8)	2 (1)	Ala -> Thr
.15	75	TCAACATCTG [T/C] GTTGGGGAGA	22 (14)	2 (1)	Silent
.34	339	AGGAACACAT [T/C] GATCTGGGTA	2 (2)	31 (16)	Silent
1128.9	483	AAATAAAAAAAAA [A/C] AAAACCC	4 (3)	4 (3)	3' UT
.10	484	AAATAAAAAAAAA [A/T] AAACCC	4 (3)	4 (3)	3' UT
1130.7	248	CCCCCTGCGG [G/T] TGAAGAACTT	25 (12)	9 (4)	Val -> Leu
.11	320	GGAATACCGG [G/T] ACCTGACCAC	26 (12)	2 (1)	Asp -> Tyr
.13	364	ACCGAGACAT [G/T] GGTGCCCGGC	15 (10)	3 (2)	Met -> Ile
.16	377	TGCCCGGCAC [C/G] GCGCCCGAGC	16 (8)	4 (3)	Arg -> Ala
.19	421	TGGAGGAGAT [C/T] GCGGTGAGCA	12 (7)	2 (1)	Silent
1131.12	502	TGGCTGACCA [G/A] GCTGAGGCC	18 (13)	2 (2)	Silent
1133.20	279	CTGAGTCTGC [C/T] ATGAAGAAGA	41 (18)	2 (1)	Silent
.35	517	CCTAATTCTG [A/G] ATATATATAT	19 (12)	4 (2)	3' UT
1135.22	301	AAAACAAGAC [T/G] GGGGCTGCTC	38 (20)	8 (4)	Silent
.23	343	CGGGCTACTA [C/T] AAAGTTCTGG	40 (18)	4 (2)	Silent
.32	438	AAGAGTGTG [G/A] GGGGGCTGT	32 (18)	2 (2)	Gly -> Ser
1136.1	13	CGCCGCTGCG [G/A] AGGGAGCCGC	9 (9)	10 (6)	5' UT
.16	190	GGAGCCGGCA [G/A] CCGACGGCAA	31 (21)	5 (4)	Ala -> Thr
.18	197	GCAGCCGACG [G/C] CAAAGGTGTC	32 (23)	5 (5)	Silent
.19	198	CAGCCGACGG [C/A] AAAGGTGTCG	21 (16)	8 (5)	Ala -> Glu
.23	243	GCCAGCGGAA [G/C] CTGCCACCT	31 (20)	5 (5)	Lys -> Asn
.24	244	CCAGCGGAAG [C/G] CTGCCACCTC	31 (20)	5 (5)	Pro -> Ala
.25	245	CAGCGGAAGC [C/T] TGCCACCTCC	31 (22)	6 (3)	Pro -> Leu
.29	283	CAACAAGAAT [G/C] CTCGCCAC	26 (18)	5 (5)	Ala -> Pro
.30	284	AACAAGAATG [C/G] TCGGCCACG	26 (18)	5 (5)	Ala -> Val
.32	286	CAAGAATGCT [C/T] GCGCCACGCT	31 (22)	2 (2)	Arg -> Cys
.41	387	TCCTGCGCAC [G/C] CAGAAGCCTG	2 (2)	19 (14)	Silent

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1137.1	3	CTTCCTTC [G/T] AGGAGGTGGCAG	2 (2)	3 (2)	5' UT
.15	331	GTGCCGAGAT [C/T] GCTCACAATG	22 (12)	4 (2)	Silent
.23	419	CAATGCCAGG [C/G] TGC GCAGTGA	13 (9)	3 (2)	Leu -> Val
.25	488	TAAAAACTGC [C/A] ATCTGGCATC	8 (8)	4 (4)	3' UT
1138.8	78	AGGAGGAGCT [G/T] CTGAAACAGC	30 (17)	2 (2)	Silent
.14	127	GCTGCGCGTC [G/A] CCAAAGTGAC	31 (15)	2 (2)	Ala -> Thr
.24	354	AGCAGCAGCG [G/T] AAGGAGCGGC	28 (16)	2 (2)	Silent
1139.21	334	TTCCGAAGCA [A/G] TCTTCCTGCT	33 (20)	3 (1)	Asn -> Ser
1140.3	17	CCGCTGCTCG [C/A] CATGTCTTCT	22 (15)	3 (2)	5' UT
.20	341	AATATGTAAG [G/A] CCTTCTTTT	32 (16)	2 (2)	3' UT
1141.5	201	ATCAGACTAG [A/T] GCTGAGTCTT	2 (1)	11 (5)	Arg -> Ser
.7	346	GCGCCGTGG [C/A] ATCGTAGAGT	4 (3)	3 (2)	His -> Asn
.18	1071	GGATAAGGCA [G/A] CTGCTGCAGC	5 (4)	6 (3)	Silent
.21	1376	TGTTATACAGGCAGTGA [G/A] AAA	14 (10)	5 (4)	3' UT
1142.13	556	CTTGTGACTG [A/G] CCTCTGGTCC	8 (7)	3 (3)	Asp -> Ala
1143.17	470	ATCTACAAGC [G/T] TGGTTATGGC	32 (20)	2 (2)	Arg -> Leu
1144.1	211	GCCGCGGGCG [G/C] CCCCTGCGCA	7 (5)	4 (4)	Silent
.5	286	CCGCCGAGGG [C/A] ATTCACACGG	11 (9)	5 (4)	Ala -> Glu
.6	287	CGCCGAGGGC [A/T] TTCACACGGG	15 (13)	4 (3)	Ile -> Phe
.17	494	TGTGAAGCTG [C/T] CCTCCGGCTC	9 (8)	2 (2)	Pro -> Ser
.26	700	ACCAGCACAT [C/T] GGCAAGCCCT	24 (18)	2 (2)	Silent
1145.18	395	GTGAAAAATA [C/T] ATCCGCAGGG	21 (14)	7 (7)	Silent
.20	405	CATCCGCAGG [G/T] TTCGGATGAG	27 (20)	2 (2)	Val -> Phe
1146.16	276	TGTTTGCAAA [G/T] GCCCTGGCCA	16 (12)	3 (3)	Lys -> Asn
.18	285	AGGCCCTGGC [C/A] AACGTCAACA	13 (10)	5 (5)	Silent
.22	340	ACCTGCTCCA [G/C] CAGCTGGTGC	16 (12)	3 (3)	Ala -> Pro
.23	341	CCTGCTCCAG [C/G] AGCTGGTGCT	15 (12)	3 (3)	Ala -> Glu
.25	343	TGCTCCAGCA [G/A] CTGGTGCTGC	17 (12)	2 (2)	Ala -> Thr
1147.22	324	GAGACTGGCA [G/A] GCCTCGGCCCT	7 (5)	3 (3)	Arg -> Lys
1148.29	390	TCGGTGACAT [C/T] GTCACAGTGG	33 (17)	3 (2)	Silent
1149.14	174	GAACCGGGGC [C/G] TGCGGCGGAA	14 (12)	3 (2)	Leu -> Val
.22	414	CGTAAAGCAT [G/T] GCCGGCCCCG	23 (20)	4 (3)	Ala -> Cys
1150.20	257	CTCAAAGACC [T/C] GGAAAAATGG	42 (19)	2 (1)	Leu -> Pro
.34	435	CCTCATGGAC [T/A] AAAAAAAAAA	7 (6)	4 (3)	3' UT
1151.13	312	TCCAAAGCCC [T/C] GGTGGCCTAT	33 (16)	6 (1)	Leu -> Pro
.14	313	CCAAAGCCCT [G/T] GTGGCCTATT	33 (16)	6 (1)	Silent
.16	346	TGGATGAGGC [T/C] TCCAAGAAGG	34 (16)	2 (1)	Silent
.22	439	AGTTTGGAGG [C/T] CCTGGTGCCC	20 (14)	6 (4)	Ala -> Val
.25	517	TAATAAACAG [T/A] TTTTGAGGGA	23 (15)	3 (1)	3' UT
1152.15	131	GCGCGTGTGC [G/A] AGGAGATCGC	34 (18)	3 (2)	Ser -> Lys
.19	160	CCAGCAAAAA [G/C] CTCGCAACA	31 (18)	6 (4)	Lys -> Asn
.20	161	CAGCAAAAAG [C/G] TCCGCAACAA	29 (16)	5 (3)	Leu -> Val
.24	184	TAGCAGGTTA [C/T] GTCACGCATC	20 (9)	22 (15)	Silent
.31	379	CCAACCTTCA [G/A] GTCACCTCAGC	36 (23)	2 (2)	Silent
1154.8	119	GGGCACAGCC [C/T] TAAAGGCCAA	17 (9)	3 (2)	Silent

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.39	477	TAGTAATAAA [T/C] TTTCATATGC	21 (15)	2 (2)	3' UT
1155.6	64	TATTCTCCGA [G/C] CTCGCAATG	29 (19)	3 (3)	5' UT
.7	65	ATTCTCCGAG [C/G] TTCGCAATGC	25 (17)	3 (3)	5' UT
1157.3	75	TGGGCAGGAC [C/G] GGTTCCTCAGG	18 (11)	3 (3)	Silent
.12	290	GTCTGTCA [A/G] TCTGCTCCTT	28 (12)	11 (7)	3' UT
1158.4	55	CGAAAATTTCG [G/A] CCAGGGTTCT	36 (20)	2 (1)	Ala -> Asp
1159.2	68	AGCACCAGCG [G/T] TGGCAGAGAC	24 (14)	2 (1)	Val -> Leu
.7	199	ACAGTGCAGG [G/A] CGGTATGCCG	16 (10)	5 (3)	Gly -> Glu
1160.10	124	TCAGGGAGCT [G/A] AATATTACGG	28 (18)	2 (1)	Glu -> Lys
.15	166	GTGGTGGTCG [G/A] AAAGCTATCA	28 (17)	2 (2)	Glu -> Lys
.17	229	TCCAAGTCCG [C/G] CTAGTACGCG	2 (2)	29 (19)	Pro -> Ala
1161.8	263	AAGGCAACGC [C/T] CTGCTGCGGC	30 (16)	2 (2)	Silent
.9	264	AGGCAACGCC [C/T] TGCTGCGGCG	22 (14)	9 (9)	Silent
.11	283	CGCTGGTCC [G/C] ATTGGGGGTG	13 (9)	4 (4)	Arg -> Pro
1163.8	1522	GTACTTCCTC [G/T] TCCTCATGCC	2 (2)	5 (1)	Arg -> Leu
1165.1	97	CCACGACCGT [G/C] GCTATCTGGT	3 (3)	2 (2)	Ala -> Arg
.4	180	GTGAGGGGCG [G/T] CCGCGGCGCA	4 (3)	4 (2)	Silent
.7	273	CCAAGGTGGG [C/A] ATCAAGACCA	10 (7)	4 (3)	Ala -> Glu
.8	274	CAAGGTGGG [A/T] TCAAGACCAT	20 (12)	3 (2)	Ile -> Phe
.13	429	AGCAGGAGCT [G/C] CTCATCAACA	8 (7)	5 (4)	Silent
.14	430	GCAGGAGCTG [C/T] TCATCAACAT	5 (5)	8 (5)	Leu -> Phe
.29	901	CCCCAGAGG [G/A] AGGTCACCTG	13 (10)	4 (3)	3' UT
.35	1007	GCTTCCTCCT [G/T] GGCCCTCAAT	6 (5)	4 (4)	3' UT
.38	1189	GATGTTTGA [C/G] GAAATAAATT	2 (2)	7 (6)	3' UT
1170.2	410	ATTGCGAATC [G/C] TTAGATATCC	2 (2)	2 (2)	Val -> Leu
1171.27	2823	AAGAGATGAA [A/T] AAAAAAAAAA	8 (6)	4 (4)	3' UT
1172.15	1519	CTCTAGTGTT [G/C] AGGGATGTAG	7 (7)	2 (1)	3' UT
.19	1784	CAGGTCTTAA [T/C] GCCTCCATAC	3 (3)	2 (2)	3' UT
.25	2423	GAGAGACTGG [T/A] GGGTCTGTCT	7 (6)	5 (4)	3' UT
1173.12	4730	AGTAGGTAGG [G/T] CTAGTAGGTA	6 (6)	2 (1)	3' UT
.01	981	GCAGCCCCAG [T/C] GCACCTGAGC	24 (18)	48 (30)	Silent
.02	1041	ACATCAAGAG [A/G] TACCTGGGCG	71 (36)	1 (1)	Silent
.03	2400	AGCTGAGTGC [C/T] GCCACCACCT	71 (36)	1 (1)	Silent
.04		4 bp deletion			
.05	2567	CTAGATAGCA [A/G] ATAGCTCTCA	71 (36)	1 (1)	3' UT
.06	2888	CCCAAGCTGC [C/T] TCATGGCCCCG	63 (36)	9 (9)	3' UT
1174.24	3200	TGTTGACAGG [G/C] TTTTAAAGAA	10 (8)	2 (2)	3' UT
.27	3302	TCTGCCCAAGC [A/C] AAAAAAAAAA	5 (3)	3 (2)	3' UT
1176.13	2571	GAGGCTTTGC [C/T] TTGCCTGCAT	6 (4)	3 (3)	3' UT
1177.18	1684	CTCTTCCCCC [T/C] AAAAAATGGTA	13 (10)	3 (3)	3' UT
.21	1864	GTTAGCTTTA [A/G] AAAAAAAAAA	5 (5)	3 (3)	3' UT
1181.8	678	TACCAAAGCA [G/A] GGGTTCCCCA	10 (7)	2 (2)	Arg -> Lys
1183.18	1719	CTTCCTGCTC [G/A] ACTGAAAAAA	14 (9)	2 (1)	3' UT
.21	1799	TGGCTTTCAG [G/C] CCTGGCCTTT	15 (10)	5 (4)	3' UT

1184.14	2292	GCCTAAATGT[G/T]TGAAGTGC GA	30 (18)	2 (2)	3' UT

1186.7	1337	GGGAGAGGTG[A/G]CCCTGAGGGA	2 (1)	4 (3)	3' UT

1188.7	1601	AGTCATCTGA[G/A]GTTATGCTTT	4 (3)	2 (1)	3' UT

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1189.13	1270	CGGAAAGGAA [G/A] CGTTGGCAGC	11 (9)	3 (2)	3' UT
.16	1341	AGCCCCAGGG [A/G] CCAATTTTCC	14 (12)	2 (1)	3' UT
1190.5	1010	GGGGTTGGGC [G/T] GGTTCCTTTG	2 (2)	3 (3)	3' UT
1193.1	79	CTCTCCCCTC [C/G] AATCCTATCC	5 (5)	2 (2)	5' UT
1196.23	2123	TATGTTTTCC [T/C] ATGCAATAGT	19 (14)	2 (2)	3' UT
1198.29	2395	TGGCAAAGTC [T/C] GAAATAGGTC	20 (15)	4 (2)	3' UT
1199.3	1012	AGATTCAGAA [C/T] ATGGTGGGGA	3 (2)	2 (2)	Silent
.13	1460	TGAGAACACC [G/C] CGCAGCGTGA	8 (7)	2 (2)	3' UT
1202.7	671	ACCATAACTT [T/C] TTTTAAAGGA	13 (7)	11 (6)	3' UT
1205.1	942	GGAGAAAATT [G/A] AAGAATATCT	13 (6)	2 (1)	Glu -> Lys
1206.3	740	ACATCACAAA [A/G] CAACCTGTGG	3 (3)	2 (1)	Silent
1208.3	1984	TATTCGTAC [G/A] TACAATGCCT	2 (1)	2 (2)	Silent
.15	3163	AATTTTTTTT [T/C] TTTTAAATTA	2 (1)	15 (6)	3' UT
1214.9	1566	GCATCCTGGA [C/T] AGCAACAAGA	5 (3)	2 (2)	Silent
1216.8	202	AGCGGAGCGC [C/G] TCCCGGACA	5 (4)	3 (2)	Silent
1217.3	2545	GCCTCTCGGC [C/T] TTTCTCCACG	5 (3)	2 (1)	Silent
.5	2688	GCCGTGTGCC [C/A] ATGCTACCTT	12 (6)	3 (3)	3' UT
1218.10	2757	GCAGGCTGCC [C/T] TTTAGAGAGG	4 (2)	2 (1)	Silent
.01	1100	GATGTCAGTG [G/C] CCCCATGCCC	71 (36)	1 (1)	Gly->Ser
.02	1287	GCCATGCACT [C/G] ACCAACGCCA	71 (36)	1 (1)	Silent
.03	3385	TTGCCTGGAC [G/A] TTGGCCTGCG	71 (36)	1 (1)	Silent
1221.20	1893	TGGAGCCTTC [G/T] GCTGGAAGTC	9 (7)	3 (2)	3' UT
1222.30	2797	CACAAACCA [A/G] TTGTAATAA	14 (11)	2 (1)	3' UT
1223.3	2813	AAGCAGGAGG [C/T] TAAGAAAGTG	13 (10)	2 (1)	N/D
.9	3662	GGACCGCAGT [C/T] CAGCATTGT	2 (2)	2 (1)	N/D
.10	3727	TAACTGAAG [T/A] GTGTTTTTCC	4 (4)	3 (2)	N/D
.15	3855	ACGTCCCAAC [G/A] AAGAGACCAC	24 (19)	2 (2)	N/D
.16	4110	CACCTTGGTG [G/A] AGAACAAAGAA	20 (17)	2 (2)	N/D
.20	4155	CGACGTGGAT [C/T] CCATCGAGGT	21 (17)	2 (2)	N/D
1224.13	1739	GCAGAGCCAC [C/A] AGGGAAGT	2 (2)	2 (2)	3' UT
.17	1936	CCTCTTCTAA [T/C] CTCAAGGTC	3 (2)	8 (7)	3' UT
.21	2061	GCGAGTGAGT [G/T] GAGAGCCAGC	15 (11)	17 (13)	3' UT
.22	2079	AGCTCTGCGG [A/G] GTCATCACGC	15 (11)	17 (13)	3' UT
1227.9	1107	AGAAGGTGAA [C/A] CCCCTGGGGG	9 (6)	4 (3)	Asn -> Lys
.16	1207	TGGGAAGAGG [G/C] CATACGAGT	20 (14)	2 (2)	Ala -> Pro
1229.18	1919	ACTCCGTGCG [C/T] AATGCCGTCA	4 (3)	2 (1)	Silent
1235.11	1194	TAGCCGCCAG [G/A] ATTGCCATGA	18 (12)	2 (2)	Asp -> Asn
1238.14	1133	AGAACCTGAA [G/A] GCTGCGCAGG	6 (4)	2 (2)	Silent
.17	1298	AACAACCTCA [G/A] GCCCTGCCCC	8 (6)	2 (1)	3' UT
1239.13	1289	ACTTTTCCTC [T/C] AATCCTGGAA	11 (5)	7 (4)	3' UT

.14 1292 TTTCCTCTAA (T/C) CCTGGAAATT 16 (7) 2' (-2) 3'-UT

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1241.13	1802	AATTAAAGTTTTTCTTC [C/T] ATG	10 (7)	2 (2)	3' UT
1242.18	3296	TCCTGTCACA [T/C] GTGCAGCAGG	13 (11)	2 (2)	3' UT
.20	3328	AGCGGGCATC [G/T] CTGCCGCCAT	7 (7)	3 (3)	3' UT
1243.5	134	GAACGCAGTG [G/A] ATGCCTTTCG	4 (4)	3 (3)	Asp -> Asn
.6	184	TGCGCAGCCC [C/G] GTCACCAACA	7 (7)	3 (2)	Silent
.7	185	GCGCAGCCCC [G/T] TCACCAACAT	7 (7)	4 (2)	Val -> Phe
.24	1528	CGGTGGAGCA [G/A] CCCCTGGGCT	10 (8)	3 (2)	3' UT
.31	1789	TACACGTGTT [G/A] CTTGCTCCAG	14 (9)	2 (2)	3' UT
.32	1790	ACACGTGTTG [C/A] TTCGTCCAGT	16 (9)	8 (7)	3' UT
1246.6	1512	ATCCCGGAGG [G/T] TCACTCTGAA	2 (2)	2 (1)	Val -> Phe
.9	1958	ACGTTTAAAC [A/G] TAGTAAATCC	3 (3)	6 (6)	3' UT
1247.6	517	GCGGACAGTA [C/T] ATTGCCATTG	2 (2)	2 (2)	Silent
1248.4	164	TGATGTCCCC [C/T] TCGACCCGT	4 (3)	2 (2)	Silent
.5	172	CCCTTCGACC [C/A] GTCGGGTTTG	2 (1)	3 (3)	Pro -> Gln
.11	815	AGCACAGCCC [C/T] TCTACCAGGG	13 (7)	2 (2)	Silent
1249.1	50	ACCGCCTGCG [G/A] AGTAAC TGCA	4 (3)	2 (2)	5' UT
.26	1800	TTGTAAAAGG [G/T] TTA CTCTCAT	26 (16)	2 (1)	3' UT
1250.1	353	GCCCCGCCAG [G/A] ATTAACACAG	3 (2)	2 (2)	Silent
1251.11	1070	CCGCCAACGG [C/A] AACATCGACC	2 (1)	4 (2)	Ala -> Glu
.18	1974	CTGGGAAATG [C/A] GGGACTGGAA	2 (1)	2 (2)	3' UT
1253.7	673	GCCAGGTGGT [G/C] CAGATCCCTG	2 (2)	2 (1)	Silent
.11	1620	GCCTATGTCG [G/A] CGACGTCCAC	2 (2)	2 (1)	Ala -> Asp
.13	1672	ACACCAGAC [C/T] ATGGAGCTGC	2 (2)	2 (1)	Silent
.16	3427	TCGACCACGC [G/A] GAGCGGGAGC	2 (2)	2 (1)	Silent
.21	3848	GACCCCGCTG [C/T] CACCCGCTTT	2 (2)	2 (1)	3' UT
1255.11	895	TCAAATGAAT [C/G] AACCACCTGG	2 (2)	2 (1)	Gln -> Glu
.23	1729	TCATTTTCT [A/G] TATAGGCTGC	2 (2)	17 (8)	3' UT
.24	1731	ATTTTCTAT [A/G] TAGGCTGCAC	2 (2)	17 (8)	3' UT
.27	1801	TTTCCAATAAAATC [G/A] GAATTC	3 (2)	3 (3)	3' UT
1257.11	674	AACAAGAACA [C/T] ATGATAAATT	9 (6)	2 (1)	Silent
.19	954	GTGAGAGAAC [G/C] AAATCTCTAT	21 (14)	3 (2)	3' UT
.20	955	TGAGAGAACG [A/C] AATCTCTATC	19 (14)	3 (2)	3' UT
1258.11	329	ATCACAGCAA [A/G] AGAGAGGTTT	22 (9)	4 (1)	Lys -> Arg
.15	357	TCACTACCAA [C/T] CTGATCAATT	24 (10)	6 (3)	Silent
.17	422	TCTGCCTTT [C/T] TACCATGATG	25 (11)	2 (1)	Ser -> Phe
.20	533	AGCTTCCTAA [G/A] TCAAGGCCAA	27 (13)	2 (1)	Ser -> Asn
.32	745	GCTTCCAGAA [C/G] AGATCAAAAA	17 (10)	2 (1)	3' UT
1261.6	425	CTGGCATCAT [C/T] GCCATCTACG	9 (3)	2 (1)	Silent
.20	908	CGCCCCCTCCA [G/A] GCCCCCGGCG	8 (3)	3 (3)	3' UT
1265.1	46	ACTCGAGCCT [G/A] CTGTTACCCG	3 (2)	2 (1)	5' UT
.19	1023	GGAGGGGGCA [A/G] ATGGTGGTTG	2 (1)	20 (7)	3' UT
1266.1	343	CGCTGCGGAC [G/A] AAAAGGCCAA	2 (2)	3 (2)	Glu -> Lys
.7	661	AGCAGGTGAA [G/A] GGCATCGCTG	7 (6)	4 (3)	3' UT
.9	671	GGGCATCGCT [G/T] CCCCAGGCCT	10 (9)	4 (3)	3' UT
.16	865	GTAGAGCACA [G/A] GGGTTTCCCC	25 (12)	2 (2)	3' UT

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1267.11	1776	GGCTAGAGGA [T/C] GCACGGTGGC	2 (2)	7 (5)	3' UT
1268.10	6529	TTCATCCTCA [C/T] TCCCCACATC	10 (6)	2 (2)	Thr -> Ile
1269.19	1893	CAACTTCAAC [C/G] TGGAGGTGCA	12 (4)	3 (3)	3' UT
.20	1941	TAAAAAGGTG [A/G] CTGTTTATA	12 (4)	4 (4)	3' UT
1270.11	331	TTGTCCTCAG [T/C] ACCTCTCCGT	11 (9)	2 (2)	5' UT
1271.14	949	GGGTGTATTA [T/C] CCAGTACTC	18 (11)	5 (1)	3' UT
1272.10	2678	TGTTAAGGAA [C/T] GCTAGCAGGG	3 (1)	3 (1)	3' UT
1273.13	3127	AAAGGAAGTT [T/C] TCCTTTTGAA	7 (2)	10 (3)	3' UT
1274.16	2696	ATATTTTTTC [A/G] TAATCTATAT	7 (6)	3 (2)	3' UT
1278.7	864	AGTGTGACCC [G/A] GACTGCCTCC	3 (1)	2 (2)	Silent
.32	3897	CCAGAACACG [G/C] CTCACGCTTA	5 (3)	3 (3)	3' UT
.33	3898	CAGAACACGG [C/G] TCACGCTTAC	4 (3)	4 (4)	3' UT
.34	4013	TGTTGTGTGT [A/G] TCGAGAGGCC	10 (7)	3 (2)	3' UT
1280.5	1648	TTAAGAGGAC [G/A] TAATGGGGTTC	14 (8)	4 (3)	3' UT
.15	1957	TAAAGATGATTGTGG [G/A] AATTC	2 (2)	9 (8)	3' UT
1282.1	2155	TTTGGTGGGC [C/T] TACTTGGTGC	7 (3)	6 (1)	3' UT
.2	2283	GTGTGGCGTA [G/C] GCAGTGGGTC	13 (1)	2 (2)	3' UT
.9	2799	TTACATCACC [G/A] CCACTACTGC	6 (3)	2 (2)	3' UT
.10	2824	CAGTGCCAG [T/C] GGCGCATGC	4 (1)	3 (3)	3' UT
.15	2937	TGGTTTGTGTT [G/C] CCTGACACAG	11 (4)	3 (1)	3' UT
1284.1	249	CTGTCGACGA [T/C] CCCTACGCCA	7 (7)	4 (3)	Silent
.6	522	GGGGCAGTGC [G/C] GTCATCTCCC	5 (1)	5 (4)	Silent
.7	523	GGGCAGTGGC [G/T] TCATCTCCCT	7 (4)	4 (1)	Val -> Phe
.10	608	GCCCTTGGGG [G/T] TTGCAGGCTG	8 (7)	2 (1)	3' UT
.20	651	GGGCTGGGG [G/A] ATCCCAGCAG	8 (8)	2 (2)	3' UT
1286.20	5366	GGCCATTGCC [G/A] CAGTCGCAGC	12 (11)	2 (2)	3' UT
1287.10	864	AGGGATGTTAGACGGAATT [C/G] C	2 (2)	4 (3)	3' UT
1289.15	885	ATCATGTGGA [G/A] GGGCCAGAGG	13 (9)	2 (1)	3' UT
.22	1006	GGCATTCCAG [C/G] TGAGACACTG	21 (10)	5 (2)	3' UT
1290.7	929	CCCTCACCCC [A/G] TCACGCCTCG	3 (1)	2 (2)	3' UT
1291.5	1060	TCAACAAAA [G/A] GGACAGGTAC	2 (1)	2 (1)	Silent
.8	2168	TAAGTACCAC [G/A] AGCAGCTGGG	2 (1)	2 (1)	Ser -> Lys
.12	4517	GCTGACAGAG [G/A] AGGAGGACTA	5 (2)	2 (1)	Ser -> Lys
.13	5114	CCAGCCTCCA [G/A] TGTACAACTT	4 (1)	2 (1)	3' UT
1292.11	3547	AGGCAAATTC [A/G] ATTTGAACAT	7 (3)	5 (3)	3' UT
.20	3888	TGTGTGTGTG [T/G] GCTGTGCTT	11 (9)	3 (3)	3' UT
.21	3889	GTGTGTGTGT [G/T] CTGTCGCTTG	11 (9)	4 (3)	3' UT
1293.10	2480	CATGCCTGTG [C/G] GTGCGCTTCC	2 (2)	3 (2)	3' UT
.11	2481	ATGCCTGTGC [G/C] TGCCTTCTT	4 (4)	2 (1)	3' UT
1298.20	960	TTCAGTGGGC [T/C] TTTCTGGCAG	12 (8)	2 (1)	Leu -> Pro
1300.7	566	AAGTGACCT [T/G] GAATTCCTTG	2 (2)	4 (2)	N/D

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1301.12	668	CGCCCGGCTG [G/C] GCAAGGAGAT	9 (5)	3 (1)	Ala -> Arg
.30	1058	CAAGGTCTAT [G/C] CTGACGCCTC	16 (7)	3 (2)	Ala -> Pro
.31	1059	AAGGTCTATG [C/G] TGACGCCTCC	13 (6)	3 (2)	Ala -> Val
1302.7	759	ACAGGCCACA [T/G] CTGGACCATC	2 (2)	5 (5)	Ser -> Ala
.8	806	TATCAACTCC [C/T] GGACAACCCA	2 (2)	4 (4)	Silent
.10	866	TTCGAAGAGT [T/C] ATTGCCAAGA	4 (4)	2 (2)	Silent
.17	2000	GAATTTAATA [G/T] GTACAGAAGT	5 (5)	4 (4)	3' UT
.19	2158	ACTTCTAAAG [C/A] AAGAGGATAA	8 (7)	9 (9)	3' UT
1303.5	1226	TGCTGTGCAC [A/G] TTGACTACAA	6 (5)	2 (2)	Ile -> Val
.15	1624	GATTATATAT [T/A] TTTTCTCTG	7 (5)	3 (3)	3' UT
.21	1813	GTGCACTAAT [A/G] TGTAAGACAA	9 (6)	3 (3)	3' UT
.22	1920	TTAAATAGCT [C/T] TTTTCTCTGA	2 (1)	14 (8)	3' UT
.23	2079	TCTATAAACC [A/G] AACTGATGTA	2 (1)	16 (9)	3' UT
1305.12	1434	AATAAACTATAGTAGTGTT [T/A] T	8 (8)	5 (4)	3' UT
1306.14	407	TTTGATATTG [C/T] CTCTGGAACCT	2 (2)	4 (4)	Ala -> Val
.21	1021	TTTTTTTGCA [A/T] AAAACTAAAT	2 (2)	4 (3)	3' UT
1309.4	466	GCGGGCCGCC [T/C] GCTCTGGAG	5 (5)	2 (1)	Leu -> Pro
.5	494	AGGAGTATGC [G/A] GCTCGGGCCC	4 (3)	3 (3)	Silent
1312.10	492	ACCCCTGGGG [G/A] AGTGCATCAT	7 (6)	3 (3)	Ser -> Lys
1315.13	339	AAGTTCCTCA [C/A] GCCCTGCTAT	13 (10)	2 (2)	Thr -> Lys
.22	766	TCCTTTTTTA [A/G] AAAAAA	8 (7)	3 (3)	3' UT
1317.4	1083	GATAGATTAT [G/A] TATTCTTCCA	3 (3)	4 (3)	N/D
1318.2	183	GGGAGCCTGC [C/A] AGGGTCCGCT	12 (11)	3 (3)	Silent
1322.12	876	TGACTCCACA [G/A] CCTCAGCCGA	23 (14)	5 (5)	Ala -> Thr
1326.5	139	GGCCTGGAAA [C/T] TTGCACAGTC	5 (5)	3 (1)	Leu -> Phe
.12	1339	TAGGAAAGAC [G/A] TCGGCTTTCG	5 (2)	3 (3)	Val -> Ile
.17	2214	TCCCCAGGGT [T/C] TTCTCATGGT	2 (2)	5 (3)	Silent
.19	2333	ATTCTGAGGG [A/G] TATCCAGCAG	4 (4)	4 (2)	Asp -> Val
1328.5	2968	CCTAAAAGTG [T/G] TTTTATTTC	6 (4)	4 (4)	3' UT
1330.13	1526	TTGATCATGA [G/A] ACATAGGTAT	6 (3)	2 (1)	3' UT
1331.15	1666	ACAAGCACAC [C/G] TTAGAGGCTT	2 (2)	10 (4)	3' UT
.24	2009	CTGCTGATGC [C/T] GTACCCCTCAC	13 (7)	2 (2)	3' UT
1332.5	618	AGCTGAACCC [G/C] GAGTCTCTCC	2 (1)	2 (1)	Silent
1333.4	89	GAGCACAGCG [G/A] CATCTTTGGC	7 (5)	2 (2)	Ala -> Asp
.10	279	CCGTGCAGGC [C/A] ATGAACCGCA	5 (5)	6 (5)	Silent
.24	756	TGACCCCGA [C/A] CCAGCCTCGC	6 (6)	7 (6)	3' UT
1335.1	331	AGGGCTGGCC [C/T] TTGGAAGGCG	4 (4)	2 (2)	5' UT
.13	872	AGCCAAGCCG [G/T] TCAAGGCATC	7 (6)	2 (1)	Val -> Phe
.28	2268	GGAAAAGGGA [G/A] AACTGAGCG	6 (6)	2 (2)	3' UT
1336.6	851	GCCGCGAGGC [C/G] TGGTCTGAGC	5 (5)	11 (5)	3' UT
.7	889	GGTCCTCTCA [G/A] TCTTTCCCT	21 (10)	2 (2)	3' UT
.15	990	TTGGCAACGG [C/T] CGTCGTCATG	17 (11)	2 (1)	3' UT

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1337.12	420	GCACTCATGC [C/G] GGGTGATCGT	32 (15)	3 (2)	3' UT
1339.17	2972	TATTAGTCCA [A/G] TGAGATTTCC	12 (9)	7 (4)	3' UT
.20	3146	GTCGGACAGT [G/T] GCTCATAGAG	6 (6)	5 (4)	3' UT
1341.3	630	CTCGTAAGGC [G/T] TCCGGTCCCC	4 (4)	6 (3)	Silent
.4	633	GTAAGGCGTC [C/T] GGTCCCCCGG	10 (9)	4 (2)	Silent
.17	896	AAAAAGGCGG [G/C] CGGAACCAA	22 (14)	2 (1)	Silent
.29	1107	AGGCTGTGAA [G/A] CCCAAGGCCG	13 (8)	2 (1)	Silent
.32	1195	AAACCCAAAA [G/A] GCTCTTTTCA	7 (5)	5 (3)	3' UT
1342.5	142	GCGCCAAAGC [G/A] AAATCCCCT	11 (9)	3 (2)	Silent
.7	227	CGCAGAGCGG [G/T] TTGGGGCAGG	4 (4)	5 (4)	Val -> Phe
.8	271	TGTTAGAGTA [C/T] CTGACCGCCG	11 (11)	4 (2)	Silent
.10	314	CGCGGCTCGC [G/A] ACAACAAGAA	8 (8)	2 (2)	Asp -> Asn
1343.17	514	GAACCAAAA [G/A] GCTCTTTTCA	7 (7)	4 (4)	3' UT
1344.2	149	GAGCGCATCG [C/G] GGGAGAGGCT	2 (2)	2 (2)	Ala -> Gly
1345.3	360	GGCGCGGTGG [G/C] GTCAAGCGCA	3 (3)	3 (1)	Gly -> Ala
1346.1	2269	CAGACTGGTG [A/G] ACGAATATTC	2 (2)	2 (2)	Asn -> Asp
.2	2407	CTCTGAGACG [A/C] TGAAGACCCG	2 (2)	3 (3)	Met -> Leu
.10	3265	TGCCGGGCTT [C/T] CCTCCGGGGG	3 (3)	2 (2)	3' UT
1347.3	107	GAAGCCGAGA [C/G] GGAAAATGTC	12 (8)	4 (3)	Arg -> Gly
.5	109	AGCCGAGACG [G/A] AAAATGTCAT	2 (2)	3 (3)	Silent
.6	111	CCGAGACGGA [A/G] AATGTCATCA	16 (12)	2 (1)	Lys -> Arg
.37	994	GGTTCTTGTT [T/G] GGGCACAGCA	16 (11)	3 (3)	3' UT
.38	996	TTCTTGTTTG [G/T] GCACAGCACA	17 (11)	4 (4)	3' UT
1349.4	351	ATCGGGATCG [T/A] GTGTTCCAGT	4 (1)	9 (5)	Val -> Ser
.9	1136	GCCCTGCACG [A/G] GCCCAGGGGC	19 (13)	3 (3)	3' UT
.10	1137	CCCTGCACGA [G/A] CCCAGGGGCT	10 (6)	11 (7)	3' UT
.11	1150	CAGGGGCTGA [G/A] CGTTCCTAGG	20 (12)	2 (2)	3' UT
1350.4	188	CCAAGCGCTC [T/C] AGGGGCTTTG	4 (4)	12 (7)	Silent
.5	275	ATGGAAGAGT [T/C] GTGGAACCAA	15 (10)	2 (1)	Silent
.10	473	GGGGCTTTGC [C/T] TTTGTAACCT	9 (8)	3 (2)	Silent
.12	770	ATGGATTGG [C/T] AATGATGGAA	5 (5)	2 (2)	Ala -> Val
1351.25	1695	GTGTGGAGAA [G/A] CCACAGGCCT	10 (7)	10 (8)	3' UT
1354.23	2233	CAACAATTTT [C/T] TATGTTAGTT	7 (6)	3 (1)	3' UT
1355.7	4296	AGCCTTCAGG [C/T] TCGGGGGGCT	2 (2)	2 (1)	Ala -> Val
.8	4778	GCGCTGATAA [C/G] GTTCATGGAA	3 (3)	3 (3)	3' UT
.10	4785	TAACGTTTCAT [G/A] GAACGCGTTG	5 (5)	2 (1)	3' UT
1358.8	2515	CAGGGCGAGT [G/C] GCATGTCTGC	7 (7)	2 (2)	3' UT
.17	2629	CTTGGCATGT [G/A] ATGGCAGCTC	20 (17)	2 (2)	3' UT
1359.3	297	ATAAATACAA [G/A] AACATTGGAG	3 (2)	2 (2)	Silent
1360.12	548	TGTAAGCTGA [G/C] CCTGGTGGCC	8 (6)	2 (1)	3' UT
1361.10	4077	CTGTCTTTCC [A/G] TTTTTCATG	14 (9)	2 (1)	3' UT
1362.9	1832	CCGCCAGGCG [G/A] ATTTTGTTC	2 (2)	2 (2)	Silent

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.11	2248	CCTATCGGCT [C/G] TTTGCAGTGG	3 (2)	3 (3)	Leu -> Val
1363.22	2874	CCGGAATCCA [A/C] AGTGCTCTGC	2 (2)	7 (5)	3' UT
1366.3	615	CGCCCATGGC [G/A] ACCAGTACAA	7 (7)	2 (2)	Asp -> Asn
.6	722	TGTACAACCT [T/C] CCCGCAGGCG	2 (2)	8 (7)	Silent
1367.18	1851	AAAAAGTAATTCCTTAAA [C/A] AT	4 (4)	4 (3)	3' UT
1368.5	2964	TCTGAGACAC [G/A] CCCCAACATG	3 (3)	2 (2)	3' UT
1372.1	276	AGATGCTAAG [A/G] TTACCTTTCC	4 (3)	2 (2)	Ile -> Val
1373.13	3855	AATATAATAT [C/T] GACACAGTGC	4 (4)	2 (2)	3' UT
1378.12	4157	TGCTGGGGCA [T/C] GCGGGGATCC	2 (2)	2 (1)	3' UT
1383.14	1832	ATCACCACCA [C/T] GTGAGTGGTA	12 (6)	4 (3)	Silent
1385.17	3454	CAGTGCTAAT [G/A] TGTGCAAGCA	7 (5)	4 (3)	3' UT
1386.31	470	GGGTGACGGG [C/G] CCATGGGGCG	5 (5)	3 (3)	3' UT
1387.5	1385	TCGGTGCACT [T/C] TCCACTCTTG	2 (2)	2 (2)	3' UT
.7	1678	CAGGCTCATC [C/A] TGGGAGCTTT	3 (3)	5 (3)	3' UT
.8	1900	CAGCCCTGCT [G/A] ACCATCTCAC	4 (4)	2 (2)	3' UT
.11	1967	GCCCCCTGGG [G/A] AGTTGGGGAA	17 (13)	2 (2)	3' UT
.15	2075	ATTCTTCTCT [G/T] GTGGCATTAG	18 (14)	3 (3)	3' UT
.17	2089	GCATTAGCCA [C/T] TCCCTGCCTC	22 (15)	2 (2)	3' UT
.22	2234	AAGAGAGAGAGA [A/G] AAAAAAAA	13 (10)	6 (4)	3' UT
1388.17	2799	CACAGAAGCA [G/C] CTAAACCAAG	15 (11)	4 (1)	3' UT
1395.4	327	CAATGTGTTA [T/C] GTAGTGCTTA	35 (17)	2 (1)	3' UT
1396.10	1887	GGCACGAGCC [C/T] TCCTTCTATA	3 (3)	3 (1)	3' UT
.12	1921	CCCCAGTGGG [G/A] ACTGAGTTAT	3 (3)	5 (2)	3' UT
.21	2403	TGACCAGGAC [G/C] CCTCTGGCCC	2 (2)	3 (3)	3' UT
.26	2579	AAAGGCTGAA [T/A] TGTCTGAAAA	10 (7)	3 (1)	3' UT
1397.23	6232	TATTCAGAGT [G/T] GGCTGGGCCC	3 (3)	2 (2)	3' UT
1399.2	177	CCCCGAGGG [G/A] ATGCCAAGAT	3 (3)	2 (2)	Asp -> Asn
.10	1136	AGGGGACAGT [A/G] ATAGCCAGCA	3 (3)	4 (4)	Silent
.16	1279	CTGCTGTAAA [G/A] GCTGCAGCCT	8 (8)	2 (2)	3' UT
1401.3	71	CCAAGAATCT [G/A] CTGCGCATGA	2 (2)	3 (3)	Silent
.17	874	TTATGTTTAT [G/A] TTTATTATGT	8 (6)	6 (4)	3' UT
.19	917	TGGAATCAA [G/A] TGTCTAAGA	8 (7)	5 (4)	3' UT
.21	1081	TCTACTTCA [A/C] AAAAAAAAAA	2 (2)	7 (6)	3' UT
.23	1083	TACTTTCAAA [A/T] AAAAAAAAAA	2 (2)	3 (3)	3' UT
1404.12	3921	TGTTGCACAC [T/C] AGCCTTACAG	3 (3)	2 (2)	3' UT
1405.15	4823	GTCCACATGC [A/G] CTGGGCGTCT	4 (4)	12 (10)	3' UT
1406.5	4618	TGCTTTCTAG [G/C] TCAGTCCCTG	5 (3)	6 (4)	3' UT
1407.5	405	CCCAGGGGGG [G/C] AGCTCCCAT	5 (4)	2 (2)	Ser -> Gln
.9	713	TCTCTCAGAG [G/A] AAGTTTTTGG	10 (7)	2 (1)	Silent

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.18	1053	GGGCAGGGAA [T/C] CCTGGAGCAC	21 (13)	2 (2)	3' UT
.21	1144	GTGGGGTGGG [G/A] TGAGTAGGAC	2 (2)	25 (14)	3' UT
1411.4	2009	GGCGTCAGAG [A/G] TGCTGGGTGA	6 (4)	7 (5)	3' UT
1414.13	930	ACATACGAAC [C/T] GCCTCCTTCC	16 (13)	3 (2)	3' UT
1415.24	1362	GTGCGATTCT [A/G] GATAAAGCCA	7 (5)	3 (3)	N/D
.26	1442	GAGAATCCCT [G/A] GCAAAGGGAG	10 (8)	3 (3)	N/D
1420.6	461	CAGCGGGAGC [G/T] TGAAGAAAGA	2 (2)	2 (2)	Arg -> Leu
.8	685	TGGTGGCAGT [G/T] TGGGCTCTCA	12 (8)	2 (1)	Val -> Leu
.9	689	GGCAGTGTGG [G/C] CTCTCAGCCA	15 (12)	2 (2)	Silent
.16	853	GCTGGCAGCT [G/T] TGAGGCTCTA	25 (19)	2 (2)	Val -> Leu
1421.8	169	AAGTATACAG [A/G] ACAGATTACA	20 (14)	2 (1)	Silent
.25	1166	GTTAGTTTTC [T/C] GGCCCGTGGC	4 (3)	3 (2)	3' UT
.26	1167	TTAGTTTTCT [G/T] GGCCGTGGCC	4 (3)	11 (7)	3' UT
.29	1275	TCTGGCATAC [C/G] GATAGGCTTA	6 (5)	14 (11)	3' UT
1422.7	278	CGGGGAACCG [G/C] CCACCATCAA	4 (3)	3 (3)	Ala -> Pro
1424.3	1012	GGGAGGATGC [T/G] CTCTCTCGCG	2 (2)	5 (3)	Silent
.4	1021	CTCTCTCTCG [C/T] GTAGCTGGAA	5 (3)	2 (1)	Silent
.7	1295	GTTTAATGCA [T/A] GGATTCGAAA	2 (2)	3 (2)	Trp -> Arg
1425.3	274	GCACTGGAGG [G/T] TTTAATTTTG	2 (2)	2 (2)	Gly -> Val
1426.2	1364	GATCACCAGA [T/C] ACCAGGGTGT	9 (6)	2 (1)	Tyr -> His
.17	2298	TCTCCAGAGT [C/T] ACTCCGTTCT	4 (4)	3 (3)	Ser -> Leu
1427.3	90	CGCCGGCTGC [G/C] CTGCAGGTGA	8 (6)	3 (1)	Silent
.4	91	GCCGGCTGCG [C/G] TGCAGGTGAC	8 (6)	3 (1)	Leu -> Val
.6	109	GACAGTTCGT [G/A] ATGCTATAAA	12 (6)	2 (2)	Asp -> Asn
.11	438	TCTTCAGGGG [A/G] CCCAATGGTG	7 (2)	2 (2)	Glu -> Gly
.23	1172	CTATTCTATA [A/C] GGAAAACGAT	10 (5)	12 (7)	3' UT
.24	1179	TAAAGGAAAA [C/T] GATTTCTAAA	21 (10)	2 (2)	3' UT
.31	1323	CAAATTATAT [C/A] ACATTTTATC	8 (3)	13 (10)	3' UT
.34	1376	GCAGAGTCCT [G/C] ATGAAAGATG	13 (7)	5 (4)	3' UT
.37	1433	GCATATAATA [C/T] ACATTTACTG	6 (2)	9 (7)	3' UT
1430.3	682	TCTTTGGGGA [G/A] TCAGATGAGC	7 (6)	2 (2)	Ser -> Glu
1431.2	79	GCCAGTGGCG [C/T] TTCGTGGACG	7 (6)	2 (2)	Silent
.6	296	TCACGCAGTG [G/C] CCAATAATCA	10 (7)	7 (6)	Ala -> Pro
1432.8	2640	AAGTTGCTTA [G/A] AGAGCCACCA	8 (7)	2 (1)	3' UT
.9	2695	GTTTTAATGC [A/C] AAGGAAATTT	12 (9)	3 (3)	3' UT
1433.7	1695	AGCCGGGCTG [C/T] TACCTGCCCA	3 (3)	2 (2)	Silent
.10	2052	CCCCTGGGTG [C/T] GGGGTGATCG	2 (2)	2 (2)	Silent
.11	2160	ATGAGTCCAC [T/C] CTGGCCTTCC	2 (2)	2 (2)	Silent
.23	2698	GGACCTTCGA [G/A] GGCCTCTGCC	4 (4)	3 (3)	3' UT
.28	2787	GTGGAGGAGA [G/A] GCCTGTGGCC	6 (6)	2 (2)	3' UT
.30	2844	GGTGGCGCAG [C/G] CTTGGTAACG	15 (13)	8 (6)	3' UT
.31	2848	GCGCAGCCTT [G/A] GTAACGCCAT	15 (13)	8 (6)	3' UT
.32	2857	TGGTAACGCC [A/G] TGGACTGCAG	16 (14)	8 (6)	3' UT
.33	2877	GCGACAATCA [A/G] TGGATGGTGC	16 (14)	8 (6)	3' UT
.34	2942	CCCTACCTGT [C/T] TTATTTTATA	17 (14)	14 (9)	3' UT
1434.15	2041	ACTGTACCTT [C/T] TATGGTTTGC	2 (1)	5 (4)	3' UT

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.17	2127	TGATTAGAAC [G/T] GGTAGCCAGT	2 (1)	5 (4)	3' UT
.18	2154	AATATTGATA [G/T] AAAAAATAAAA	2 (1)	5 (4)	3' UT
1437.16	2825	AGTTTAAGAT [G/C] ACTTGACCCC	5 (4)	3 (2)	3' UT
.19	3129	CATGCGTAGC [C/T] TCTTGTCTTA	7 (5)	3 (2)	3' UT
1440.5	940	AACCTCAGAA [G/A] GCCAGTGTGTG	2 (1)	3 (3)	Silent
.6	1327	TGGCCCTGCC [T/C] GGGAGCCGC	2 (1)	2 (2)	Silent
.9	1906	GACCTGAAGG [C/T] GAACGTGATA	2 (1)	2 (2)	Ala -> Val
.14	2282	TCTTAGAGGC [C/T] TTTCTTGTAT	2 (2)	3 (3)	3' UT
1443.4	1943	CTTCGTGCCA [G/A] AACCTGAGAA	3 (2)	2 (1)	Glu -> Lys
1444.31	1905	CCAACAGCCT [C/T] CAAAGATGGG	3 (2)	28 (20)	3' UT
1445.4	425	CCAGGCTTGC [C/A] AGCCGAAACG	8 (5)	2 (2)	Pro -> Gln
.25	1281	AACAAAGAAA [A/T] AAAAAAAAAA	5 (4)	4 (4)	3' UT
1446.3	1227	AGGTGTGGAA [C/T] ACCCTCAGCG	2 (1)	2 (2)	Silent
.17	3090	TTATTATAT [T/C] TTTAACATAA	10 (7)	2 (2)	3' UT
1447.8	2681	GGCAATAGCA [A/G] TCTTGGCTGA	3 (3)	3 (2)	3' UT
1448.2	521	AGAAGACCAC [A/G] ATGCGAGATG	3 (2)	3 (1)	Silent
.3	587	GTCATGCTCT [T/C] GCACTTTACA	4 (3)	3 (1)	Silent
1449.20	1261	TGCGTAATGC [G/A] GCCGAAGAGC	4 (3)	21 (13)	Silent
.28	1447	CTGAGAGCCC [C/G] AGGCGTCCGC	21 (14)	2 (1)	3' UT
.31	1652	TGCGAGATTG [A/C] ATAAAAAAAA	8 (6)	6 (4)	3' UT
.32	1653	TGCGAGATTGA [A/T] TAAAAAAAAA	11 (7)	3 (3)	3' UT
.33	1654	GCAGATTGAA [T/A] AAAAAAAAAA	6 (6)	4 (4)	3' UT
1450.2	156	CCCCATGGCG [G/A] CCGCCAAGGA	11 (9)	2 (2)	Ala -> Thr
1451.13	200	GATGAGCGTG [A/T] TTCCTCTCGA	3 (2)	31 (20)	Asp -> Val
.14	201	ATGAGCGTGA [T/A] TCCTCTCGAT	3 (2)	31 (20)	Asp -> Glu
.18	417	AAGTTCACAT [C/G] AACCTCATGG	2 (1)	28 (18)	3' UT
1452.12	1659	GTACCAGAGG [C/T] ATGCCATCA	4 (4)	2 (1)	Ala -> Val
.18	2410	ATTTAAGGAC [G/A] AGACCAGCAG	3 (3)	9 (5)	Silent
.19	2419	CGAGACCAGC [A/G] GCTAATCCAA	9 (8)	3 (1)	Silent
.23	2717	GTTAATGATG [T/A] TAATGATTTT	17 (13)	5 (3)	3' UT
1454.3	338	AGGGCTTTGC [C/T] TTCGTTCACT	3 (2)	6 (2)	Silent
.7	1211	CATGCTCACT [G/T] TTCTCCCAT	9 (6)	2 (1)	3' UT
.8	1391	GTTTTTAAAAAAA [A/T] AAAAAA	3 (2)	3 (3)	3' UT
1455.6	294	CCAGGCCTTT [G/T] TCATCTTCAA	9 (8)	2 (2)	Val -> Phe
.22	911	CAGCTCGCGA [T/A] GCCCTGCAGG	13 (12)	3 (3)	Asp -> Glu
.23	912	AGCTCGCGAT [G/T] CCCTGCAGGG	8 (8)	4 (4)	Ala -> Ser
1460.1	6	AATTC [C/G] CAGAGCAACATGCCC	5 (5)	3 (3)	5' UT
.30	547	GTTCTGCTTC [A/C] CCAGGAGATC	25 (17)	5 (3)	3' UT
1461.5	154	TCCCCGGGGG [G/C] CTTTGGATCG	8 (7)	2 (2)	Silent
.32	1463	GTGTTACTGC [A/G] TTTTGTACAA	14 (8)	11 (8)	3' UT
1463.3	761	CAGCGTGGGG [G/T] TGGCCACTCC	2 (1)	2 (2)	3' UT
1464.3	21	GCCTGCAGGC [C/T] TCCCAGGAG	6 (3)	2 (2)	Silent

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.4	130	GCAGACTTAT [A/G] AGGTTGACCT	3 (1)	11 (7)	Lys -> Ser
.5	132	AGACTTATAA [G/A] GTTGACCTTA	3 (1)	10 (7)	Silent
1465.4	897	AGTTCCACCC [T/C] ACAGGCATAT	2 (2)	3 (3)	Silent
.5	1044	TGTCTCGGTC [C/G] ATGACTCTGG	4 (4)	2 (2)	Silent
.12	1758	GAGCAGAGGC [A/G] CGGAAGGAGT	8 (8)	3 (3)	Silent
.30	1892	ACCCTGTCTT [A/T] TGTGGACGTT	19 (17)	6 (6)	Tyr -> Phe
.34	1938	ATAGACCCGT [G/A] ATCGACAAAA	16 (15)	9 (9)	Silent
.37	1975	CTGTGCCACC [G/A] TCCCGCCAGC	21 (20)	6 (6)	Val -> Ile
.38	1980	CCACCGTCCC [G/C] CCAGCCATTC	21 (20)	5 (5)	Silent
.41	2014	AGACAAGATG [T/C] GGTGATGACA	22 (20)	5 (5)	3' UT
.42	2102	TTCTGCACTC [T/C] GGGGAAGAAG	23 (20)	8 (7)	3' UT
.45	2139	GATTGGCACC [T/C] AGTGGCTGGG	24 (20)	7 (6)	3' UT
1467.9	2297	CATGGAGGCA [G/A] CCAGGCCCGT	4 (4)	2 (2)	Ser -> Asn
.11	2353	TAATAATATG [T/C] ATGCCTGGGG	3 (3)	2 (2)	Tyr -> His
1471.4	3042	CACCCAACCT [G/A] TCCTTACTCA	2 (2)	3 (1)	3' UT
1473.9	390	GAAAAGCTGC [C/T] ATTCTCAAGG	13 (11)	5 (3)	Silent
.10	399	CCATTCTCAA [G/A] GCCCAAGTGG	11 (8)	3 (3)	Silent
1474.1	8	TCT [G/A] AACGGAGAGCGTAGTGA	13 (10)	4 (3)	5' UT
.2	9	CT [A/T] ACGGAGAGCGTAGTGACC	14 (11)	3 (3)	5' UT
.9	94	GCGAGAGGAG [G/T] AGGAATTTAA	27 (14)	2 (1)	Ser -> ***
.24	370	GCGGAACCCG [C/T] TCATCGCCGG	21 (15)	3 (2)	Leu -> Phe
.26	392	AAGTAGGGGC [C/A] GCCTGTCTGT	28 (14)	2 (1)	3' UT
1476.6	230	CACAAGTGCC [C/T] TTCGAGCAGA	12 (9)	2 (2)	Silent
1477.20	1470	ATTTGATGGA [G/C] GCTGCGCCGG	31 (12)	6 (4)	Ser -> Asp
.24	1480	GGCTGCGCCG [G/C] AGTGAAGAGG	34 (14)	2 (2)	Ser -> Gln
.28	1647	TTCTGTGTA [A/T] AAAAAAAAAA	9 (6)	3 (2)	3' UT
1478.19	838	TATGGAAGTA [G/A] CTCCTCAGAG	17 (11)	2 (2)	Ala -> Thr
.29	1009	TCCTCAGCTC [C/T] CTGCTGTGTT	26 (18)	2 (1)	3' UT
.30	1095	AATAAACTCTTAAAGA [G/A] CCTT	2 (2)	24 (16)	3' UT
1480.17	913	AAGAGGCACT [G/T] TAGCAGCTGC	17 (13)	2 (2)	Val -> Leu
.18	939	TGCTGCGAC [T/C] GCCAGTATTG	18 (13)	2 (2)	Silent
.19	979	CCCACCAGGA [C/A] GGGGCACTCC	17 (12)	4 (4)	Silent
.20	980	CCACCAGGAC [G/C] GGGCACTCCG	11 (10)	4 (4)	Arg -> Pro
.29	1113	TAGGCATGCC [G/C] CCTCCGGGAA	20 (13)	2 (2)	Silent
1483.12	1969	ACTTCTCCAT [C/T] CGGTCCCTAG	2 (1)	2 (2)	Silent
1484.2	140	ATTACGATGA [G/A] GAGGAAGAGC	3 (2)	12 (8)	Ser -> Glu
.7	288	CTGTGGCTTG [G/A] AGCATCCTTC	8 (7)	2 (2)	Ser -> Lys
.11	674	AGCACTTTGT [G/C] CTGGACGAGT	3 (3)	2 (2)	Silent
1486.24	6427	GCATTAACTA [A/T] AAAAAAAAAA	5 (5)	7 (5)	3' UT
1487.15	2896	GCGCCAAGCC [C/A] AGCAGGCTAC	3 (3)	3 (1)	Pro -> Gln
.20	3303	AGCCACGGGC [G/T] TCCTACTGAG	8 (7)	3 (3)	Val -> Phe
.22	3394	CTGGGAAGC [T/C] CCTGGAAGCC	11 (10)	2 (2)	Leu -> Pro
1489.14	1419	ACTCAACTCA [C/A] GGTACAAGAC	7 (5)	3 (3)	3' UT
1490.6	443	AGGCTGCTCG [T/C] GTTGCTATTG	2 (2)	2 (2)	Val -> Ala
.31	1710	CTCGTGATGC [A/G] TCTACAGTTA	11 (7)	19 (12)	3' UT

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.33	1824	GTGGGGGTAC [C/T] ATCTCAACTG	7 (4)	13 (9)	3' UT
1491.21	1488	GCATATGGGA [G/C] CCATTGGCTG	11 (8)	2 (2)	Ser -> Asp
.31	1826	TGTAAGGTTT [C/T] CATTAGTTT	28 (16)	3 (1)	3' UT
1495.3	391	CAAAAACCCC [G/A] CCGCTCCAA	3 (2)	3 (2)	Silent
1496.5	3017	AATAATAACC [A/G] AGACTTTTCA	6 (4)	2 (2)	3' UT
.15	3932	CTGCCTGGCC [C/T] TTTTCTTTC	3 (1)	6 (5)	3' UT
1497.13	1332	GCCCCATGTC [G/A] CTGGGTGGGC	3 (2)	5 (5)	Silent
.14	1338	TGTCGCTGGG [T/C] GGGCGGCACG	3 (2)	5 (5)	Val -> Ala
.16	1508	GCCACGGCGG [C/T] CGCCAGCGAG	8 (4)	2 (2)	Ala -> Val
.20	1608	CCCCCGGGC [C/G] CGGACCAGCC	6 (4)	5 (3)	Silent
.23	1713	AGCGGCTGCG [G/T] GTCCGTGACA	6 (3)	3 (2)	Silent
.39	4022	GGCTTCCCCT [G/A] CGCCCTGGGA	3 (2)	6 (5)	3' UT
.43	4187	AAACAGCAGT [T/C] CCTGGGAACC	12 (10)	2 (1)	3' UT
.44	4254	TTTCAAAAA [T/A] TTTTITAAA	2 (2)	11 (9)	3' UT
1498.5	167	GGCGTGCTGA [G/C] TGCCCTGGGA	8 (4)	3 (3)	Ser -> Thr
1500.16	2206	GAAGGAAACA [G/A] TGCAACAGCA	16 (13)	2 (2)	3' UT
.18	2310	GTTGTAAAGA [G/T] TGGGGGAGAG	25 (18)	2 (1)	3' UT
.23	2426	TGCCAAGCTG [G/A] ACGGCACGAG	10 (7)	4 (4)	3' UT
1501.5	388	GCGCTGTGCG [G/T] TGTCCCGTTC	2 (2)	2 (2)	Silent
.16	1238	CCCCGGGAGG [G/A] AGCTGACTGA	8 (8)	2 (2)	3' UT
1505.9	3934	TTAGTCATTC [T/C] AAAAAACACC	6 (4)	4 (4)	3' UT
1507.2	130	CCCCGAGGCG [A/T] TCGTGGAGGA	3 (3)	3 (2)	Ile -> Phe
1508.19	5111	CATCGCCGAG [G/C] CCTGGGCCCCG	12 (10)	3 (2)	N/D
1510.6	1066	CAAAGGAGCT [T/C] GAAGGATATT	2 (2)	5 (5)	3' UT
.8	1136	TCTAAAAGAA [A/G] AAGGAAC TAG	3 (2)	2 (1)	3' UT
1511.10	222	CTACAATATT [C/G] AAAAGGAGTC	18 (11)	2 (1)	Gln -> Glu
1514.6	103	CGGGGCTGCG [G/A] CCGCCCGAGG	11 (5)	4 (4)	5' UT
.24	624	GGCATCGTCA [G/A] AAGGAAGGGA	13 (5)	6 (5)	3' UT
.35	879	GCTGTAAAT [T/C] ATAACTTTT	27 (12)	2 (1)	3' UT
.38	913	TCCCCCAGGG [G/C] CGAGTTCCTC	25 (11)	3 (2)	3' UT
.39	914	CCCCCAGGGG [C/G] GAGTTCCTCG	20 (11)	3 (3)	3' UT
.43	1069	AGACCCAGG [G/T] CAGCATCTCG	21 (9)	5 (4)	3' UT
1515.6	175	CATGCTAGCA [T/G] GGCCTAATGA	3 (2)	9 (8)	Trp -> Gly
.28	855	CTGGAGAGCT [T/G] GGCTTCCGCG	15 (11)	4 (4)	Silent
.30	858	GAGAGCTTGG [C/G] TTCCGCGCTT	6 (6)	7 (5)	Ala -> Gly
.38	1146	ATAATAAAG [T/A] TTCATTTGCA	2 (2)	23 (14)	3' UT
1517.9	742	AATCATAATG [G/C] TTCTCCCTT	6 (3)	2 (2)	Val -> Ala
.16	1424	AAGTTATTGG [C/T] AAACGAGGTT	11 (7)	3 (3)	Ala -> Val
1518.8	947	AGAGCTGAGC [G/A] AGTTCACCAC	5 (4)	2 (2)	Ser -> Lys
1519.15	1209	CCATCAAAG [C/T] TTTGAGAATT	2 (2)	6 (5)	Silent
1520.12	6696	CAGCCTCATC [G/A] ATCCCAAAC	5 (2)	3 (1)	Asp -> Asn
.13	6806	TGCGCGGAG [C/A] AAAC TGCTCT	2 (1)	3 (1)	Ser -> Arg

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1521.6	851	AGACTCTGAG (G/C) CCTGGTGTGA	7 (6)	2 (2)	Arg -> Ser
.10	976	TTGGGAATGG (A/G) TATCAGAAGA	15 (8)	4 (1)	3' UT
.15	1165	TCACCTATAC (A/G) TTATTTAAAT	20 (8)	4 (1)	3' UT
.17	1236	GAAACTGTG (C/A) AATTGTGTGC	7 (4)	3 (1)	3' UT
1523.7	417	CACCACGGTG (C/T) TGGAAATTGTT	9 (8)	3 (3)	Silent
1524.13	2996	AAAATGACAT (T/G) AGTTTGA AAAA	3 (2)	3 (2)	3' UT
.22	3384	AACAGCTTTT (A/T) GGCCAAGCTG	20 (9)	4 (4)	3' UT
.23	3385	ACAGCTTTTA (G/A) GCCAAGCTGG	16 (7)	6 (5)	3' UT
.25	3397	CCAAGCTGGC (C/T) TGACGGTATG	25 (11)	4 (3)	3' UT
.26	3398	CAAGCTGGCC (T/G) GACGGTATGG	25 (11)	3 (2)	3' UT
1526.6	2476	TGGAGGTGCA (T/C) AACCTACTTA	2 (1)	2 (1)	Silent
.7	2715	GTGAAAGGGG (A/C) CGTGTACTCT	2 (2)	3 (1)	Asp -> Ala
1528.6	770	CCAAAAGGAA (G/A) TGAATCAGCA	2 (2)	2 (2)	Val -> Met
.10	2396	GCAGTGCGCA (A/T) TCCTGGACCT	1 (1)	4 (4)	Val -> Phe
.26	3317	TTCAAGTGAA (G/C) ATGCTGAAAG	12 (8)	7 (6)	Asp -> His
.32	3598	TATAATTAGT (T/C) ATGACAGCCA	19 (16)	2 (1)	3' UT
1530.8	427	ATCCGCCCCC (A/G) CGAGCTCCCC	4 (3)	2 (1)	Thr -> Ala
.13	894	TGCTGAACGA (G/A) CCCCTGGGG	8 (5)	2 (1)	Ser -> Glu
.30	1579	AGTCCTGAAA (G/A) GCCCAAGGCC	4 (3)	7 (6)	3' UT
1532.6	496	TCGTGCGCAA (C/T) GTGCCCTGGG	4 (2)	6 (3)	Silent
.10	963	CTGGCCTTAT (G/T) CCCAGGCCTG	6 (4)	2 (2)	Cys -> Phe
1533.12	2092	GTATCCAGG (A/G) CACACAGGAA	3 (3)	2 (2)	Asp -> Ala
1534.4	264	CCGTGCCGGC (A/T) CTTCAACATC	2 (1)	5 (4)	Silent
1536.22	6641	TTAGATATAT (A/G) TATTCATTCT	3 (3)	4 (3)	3' UT
.24	6779	ATTTTATTG (G/A) GCCCAAAAAC	2 (2)	11 (8)	3' UT
.28	7097	AGTGAATGT (T/A) TAAAAA AAAA	4 (3)	4 (3)	3' UT
1537.5	871	AGGGCAGTGC (C/A) ATTGATAGGA	7 (6)	3 (3)	Silent
.10	1466	GCAGGCATGC (C/A) AGTCTCTGCC	7 (7)	3 (3)	3' UT
1538.21	938	CCTCCACCTT (T/C) GACGCTGGGG	14 (7)	3 (2)	Silent
1539.1	67	TCGCGGCCTA (G/C) CTTTACCCGC	3 (3)	2 (1)	5' UT
.3	304	TCGATGGCTC (T/C) AGTACTTTAC	4 (4)	4 (3)	Silent
.9	1075	GTAGCGCCAG (A/C) CTACGCATTC	2 (2)	3 (2)	Arg -> Ser
.16	2048	CAAGGAAGTG (G/A) TTCTTAGATG	8 (7)	4 (2)	3' UT
.21	2718	GCCTAACATAA (A/G) AAAAAA AAAA	8 (8)	3 (3)	3' UT
1541.1	4123	TGGCGAGGGG (G/C) CTTGACGGCG	2 (1)	2 (2)	3' UT
1543.4	319	GCACCGGAAG (G/A) AGGCGCTGAC	6 (5)	2 (2)	Ser -> Lys
1544.3	534	TTGAGCCCAA (C/G) TGCTTGGACG	2 (2)	7 (4)	Asn -> Lys
.4	543	ACTGCTTGA (C/T) GCCTTCCCAA	4 (4)	7 (4)	Silent
.8	643	ACCTGTGTTT (T/A) CAAAGATGGC	12 (8)	3 (3)	Ser -> Thr
.12	728	GCTGCCAGG (C/G) TGTGCAGCGC	12 (11)	4 (1)	3' UT
.21	902	AACATCCCCT (C/T) CCATCATTAC	5 (4)	4 (2)	3' UT
.22	986	CTGCCTGGCC (C/T) CTCGCCTGTG	5 (4)	2 (2)	3' UT
1545.4	1470	CGGTGAGACC (G/A) TTGCCCGCTG	2 (1)	2 (2)	Val -> Ile
1546.1	172	CTCTGAAGAC (A/T) TGGAGATACT	3 (1)	3 (3)	Met -> Leu

Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1547.17	976	TGCTTTAAAG (G/A) GCCTGCCTGG	13 (10)	2 (2)	3' UT
1548.3	1209	CATTATTGGC (C/T) TCATCAAACC	3 (3)	3 (1)	Leu -> Phe
.4	1286	TGAAAGGTGT (A/G) AATAAGTTAC	2 (2)	3 (2)	Silent
.8	1904	ATACTAAGA (C/T) TTCTGTGCAT	6 (3)	5 (3)	3' UT
1550.7	797	TGGACGCCTT (T/C) CCAAACTGGA	2 (2)	5 (2)	Silent
1551.12	2215	CGAGACCATC (T/C) TGGCCCCCTCC	3 (1)	10 (9)	3' UT
.14	2242	TGCCTGAGCC (T/C) AGGAGCTTGA	3 (1)	9 (8)	3' UT
.15	2341	ACTGGGTCTC (G/A) CTCCGAGTGG	3 (1)	9 (8)	3' UT
.16	2372	GGAGGGAGGG (T/A) CAGGGGAGG	3 (1)	9 (8)	3' UT
1554.12	834	GGGACTTTAT (C/G) GATTGCTTCC	6 (5)	2 (1)	Ile -> Met
.14	999	ACCCAGAGGT (C/G) ACAGCTAAAG	8 (6)	2 (1)	Silent
.23	1539	ATCTGGCTGC (T/C) GATCTGCTAT	5 (4)	5 (4)	3' UT
1555.5	424	TATGGATGCC (A/G) AGCACCACAA	17 (8)	3 (1)	Lys -> Ser
.9	515	GCCAGCACCA (G/C) CCAGGAGCTG	17 (7)	3 (3)	Ser -> Thr
.30	1088	TCCTCGGCTG (C/A) GTTCAGTCTT	2 (2)	8 (5)	3' UT
1556.7	2037	TGATCTTTGC (C/T) CCTGGTATGC	5 (5)	5 (3)	3' UT
1560.7	2335	GCATTCAAGA (C/T) GGATACAGAG	5 (5)	2 (1)	Thr -> Met
1561.1	90	CTGTGCTGCC (C/T) GGCTCCCCCA	2 (2)	2 (2)	Silent
.5	373	CCCTGACATC (A/G) TGGAGTTCTG	2 (1)	2 (2)	Met -> Val
.22	1250	TGTTTCCTTT (T/G) GGGCTCAAAG	8 (7)	4 (4)	3' UT
.23	1251	GTTTCCTTTT (G/T) GGCTCAAAGC	7 (6)	4 (4)	3' UT
1562.14	540	ATTGTGCGAC (C/T) TCCTACACCT	21 (9)	2 (1)	Silent
.30	799	AGCCATGAGT (G/T) GGGCTGGGCC	14 (7)	3 (3)	Gly -> Trp
1563.10	3076	ACTCCCCTTC (A/G) TGAACCAGA	2 (1)	2 (2)	Met -> Val
1564.7	339	CTTTGGAAAG (T/C) GTGAAAGCTG	15 (10)	2 (1)	Silent
1566.2	53	GCAGGCACAG (T/C) GTCACCTTCG	2 (1)	2 (2)	5' UT
.4	175	TCCTGGCGGC (G/A) CCTCGTGTGC	3 (1)	4 (4)	Arg -> His
.10	791	GCACTGAATCC (C/T) GGCCAGGCG	3 (1)	4 (4)	Silent
.23	1741	TGCACTCTGT (G/C) CTCGCCCAA	3 (2)	3 (2)	Cys -> Ser
.24	1742	GCACTCTGTG (C/G) TCCGCCCAAG	3 (2)	3 (2)	Cys -> Trp
1567.2	1083	GGAATACTGG (G/A) AGAATCTTCG	5 (3)	2 (1)	Ser -> Lys
1571.4	1480	AGAGAAAATT (G/A) GGGAAAAGGT	4 (4)	3 (2)	3' UT
.14	2087	TCTGTCTGGT (G/A) TGGTATGAAT	5 (5)	4 (2)	3' UT
1576.13	1777	CGCCCCCTCC (C/T) CCTCTGGCCC	3 (2)	2 (2)	3' UT
.16	2031	AATTGTACATTC (C/T) CTGCATCC	3 (2)	2 (2)	3' UT
1577.10	3022	TGCCGGCCGG (A/G) ACCCAGCGGC	2 (2)	6 (5)	Asn -> Asp
.15	3229	CACACCACCG (T/C) CCTCTCGCT	2 (2)	5 (4)	3' UT
.33	3859	GGTAGCCACC (G/A) CCGGGGCACT	18 (13)	4 (3)	3' UT
.38	3980	CTGATGCATC (G/A) TTTTCTTTGC	18 (14)	4 (3)	3' UT
.47	4049	GCCAGGCCAT (G/T) GCCAAGGGGC	7 (6)	3 (3)	3' UT
.50	4055	CCATGGCCAA (G/A) GGGCCAGCTG	5 (5)	5 (5)	3' UT
1578.5	178	TACTTCGACC (G/A) CAAAAGACGA	7 (7)	2 (2)	Arg -> His
.12	451	CTTCCACCAC (C/T) AGTGTTCCAG	8 (6)	3 (2)	Pro -> Leu

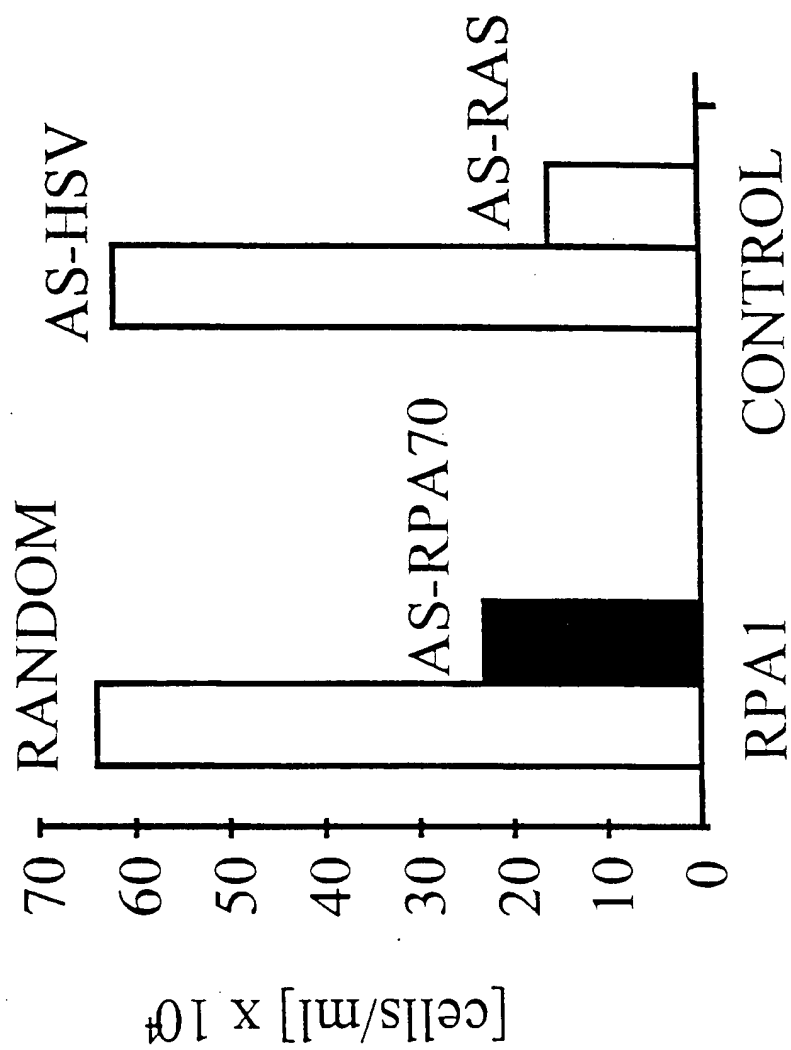
Target ID	Loc'n	Sequence around [polymorphism]	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
.13	468	CCAGATGCTT [C/T] TGACTAAGCT	8 (6)	3 (2)	Silent
.15	501	TCAGAGAATT [G/C] TAAGTGCTCA	5 (5)	2 (2)	Val -> Leu
.17	551	AAACAAATGT [C/T] AACATAATAA	5 (5)	4 (3)	3' UT
.19	630	GGGCAAATAT [G/C] CTGTATTATGA	7 (6)	2 (2)	3' UT
.20	683	CTTTGTGTAG [A/G] TCCATTGTGC	9 (7)	2 (2)	3' UT
.25	2725	AGGTGAGAAC [A/G] AAAAAACCCC	6 (5)	3 (3)	3' UT
1579.15	1735	GCTGCAGCGG [C/T] TGGCAGACGG	17 (12)	2 (2)	Silent
.19	1881	GGATCCGAGA [G/A] GGCATGGCCG	14 (12)	5 (5)	Ser -> Glu
.26	2010	GAATACTCCC [G/C] GCCAGGGCCT	12 (10)	17 (10)	3' UT
1581.2	1897	CCGCTAAAT [G/A] AGAATAAGGT	3 (3)	5 (4)	Met -> Ile
.5	2232	TGAATGTAAC [T/C] GCTTTAAGAA	3 (3)	5 (5)	3' UT
1583.7	1482	AAGACACAGA [A/T] GGAGGGCCCA	5 (5)	3 (2)	Glu -> Asp
.11	1772	GCTTTTAATA [G/C] TGTCAATAAG	3 (3)	2 (2)	3' UT
1584.18	576	CGCCCTCACA [G/A] CCTCCTTCTG	2 (2)	2 (2)	Silent
.34	1098	ATATGGATGG [C/T] GGTACCTTCA	3 (3)	2 (2)	Ala -> Val
.46	1708	GAGAAACCCC [C/T] GGGGACCATG	3 (3)	2 (2)	3' UT
.50	1848	GAGGGATTGA [G/A] CACAGGCACA	2 (2)	6 (6)	3' UT
.51	1857	AGCACAGGCA [C/A] AGAGGTGCTG	2 (2)	6 (6)	3' UT
1587.11	1330	GCCTGCGTGG [G/C] AACTCATGCA	7 (2)	11 (10)	Glu -> Gln
.12	1356	TCCAGAACCC [C/T] GACTTCCCAC	18 (14)	2 (2)	Silent
1588.26	1956	TTGTACACAA [T/C] CTCATTTCAT	7 (6)	4 (3)	3' UT
1590.2	172	TGCACGCAGC [C/A] ATGGCTGACA	6 (3)	2 (2)	Silent
.7	547	CGCTGGATAA [C/T] GCCTACATGG	8 (4)	2 (2)	Silent
.9	850	TCATCCGCAA [G/A] GCATCTGATG	4 (2)	2 (2)	Silent
.33	2139	AGCCGACTCT [G/T] GCCCTGGCCC	14 (9)	4 (4)	3' UT
1594.10	1730	ACCCAGTGG [G/A] AACTGTGCAA	6 (5)	2 (2)	3' UT
.13	1975	GAAACTAACT [C/T] GGTGGCCCCA	6 (5)	9 (6)	3' UT
.14	1985	CGGTGGCCCC [A/G] ACAGGTCTTC	6 (5)	9 (6)	3' UT
1596.3	1773	TGATGTGGTA [C/T] GTCCTCCAC	10 (7)	3 (2)	3' UT
.6	1844	GTATTCACCA [A/C] GCATTTTAGG	10 (8)	4 (3)	3' UT
.11	1899	GCATTACAA [G/A] GCACTGCCAA	17 (12)	3 (3)	3' UT
.12	1900	CATTTACAAG [G/T] CACTGCCAAA	19 (12)	2 (2)	3' UT
.16	1949	AGAGGACCTG [C/T] GGGCTTAGAT	24 (16)	2 (1)	3' UT
1598.3	2042	ATGCCTAAGA [C/A] CAACTGCGTT	2 (2)	3 (1)	3' UT
1603.5	592	TCTGTGGCAC [T/C] GATATGACCA	2 (2)	2 (2)	5' UT
.16	2566	TGAAACTGAG [G/C] CCCATCCTCA	17 (12)	2 (2)	Arg -> Ser
.18	2662	CGGGGAAGC [T/G] GCCGTCTAAA	13 (11)	3 (3)	Silent
.28	2953	TTAGAATTTT [C/T] CTAAAAATAA	26 (18)	2 (1)	3' UT
1605.14	2879	AACACGGCCC [T/C] GCTGTGCTG	2 (2)	2 (1)	Leu -> Pro
.30	4011	AATTTAAAGT [A/C] TTCTCCTCCC	4 (2)	6 (6)	3' UT
1607.13	2354	CTTTCTCTGG [C/T] CCTGTCCATG	9 (8)	2 (2)	3' UT
1608.3	2120	CAGCCGCCAT [T/C] TGCAAGGAAG	2 (2)	2 (2)	3' UT
.11	2552	CAAAAGATGA [G/T] TCCTTGCTTC	16 (9)	4 (3)	3' UT
.17	2733	TCCTAAGCAG [T/C] CCTGGCTTTT	25 (11)	3 (3)	3' UT
.01	2091	CTCCTTCCAA [C/T] CCCACTCCCC	65 (36)	7 (7)	3' UT
.02	2120	CAGCCGCCAT [T/C] TGCAAGGAAG	25 (18)	47 (40)	3' UT
.04	2578	GAAATAAAAG [T/G] AGCCAGCTG	26 (19)	46 (29)	3' UT
.05	969	AACCTAGTGC [G/A] ACCAAGGGAA	69 (36)	3 (3)	Silent

.06	2174	CCTCTCCCAG [C/T] GGCCTCCCC	71 (36)	1 (1)	Silent
.07	2129	TTTGCAAGGA [A/G] GGCCTAATCA	66 (36)	6 (6)	Silent

1611.20	1388	AACACTGGTGCCAACCAA [G/A] AC	3 (3)	3 (3)	3' UT

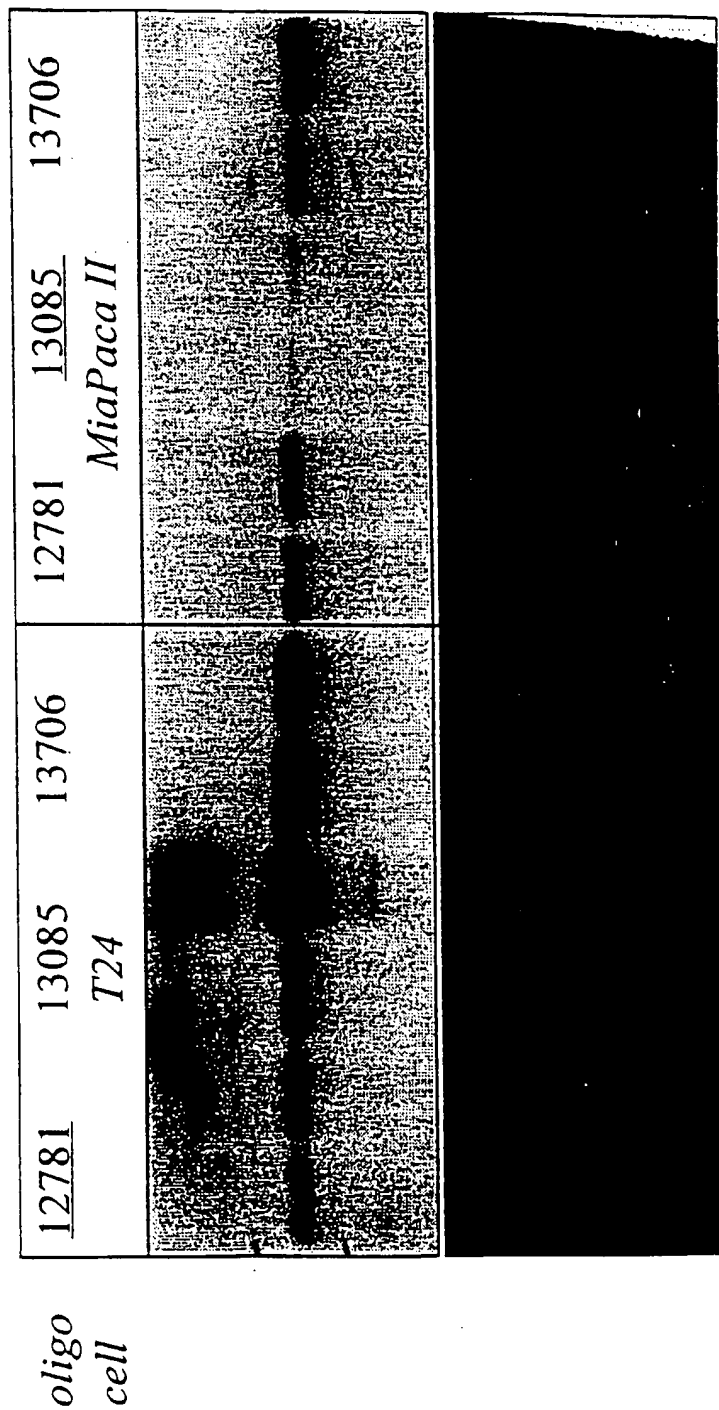
Target ID	Loc'n	Sequence around (polymorphism)	# Varia 1 (Lib)	# Varia 2 (Lib)	Protein Change
1613.2	350	AGTGGCCATG (G/A) TTGGGTCAGC	10 (7)	3 (3)	Val -> Ile
.11	842	TGATCATCAT (T/C) TCCTTGCGGA	3 (3)	6 (4)	3' UT
1614.5	1343	CCTATCTGGA (T/C) ACATTGGCC	2 (2)	3 (3)	Silent
.13	1841	CGGCGGTGGA (G/A) GCTGAGCGCC	10 (9)	2 (2)	Ser -> Glu
.23	2158	TTTTTTTTT (T/A) AAAAAAGAAA	7 (7)	8 (5)	3' UT
.28	2261	CTGAAGTCTA (G/A) GATATTTTTC	5 (5)	2 (2)	3' UT
1615.25	2113	CCTGGCCATC (T/C) TGGGCAGTGT	16 (11)	7 (5)	Silent

Fig. 9



Variance Specific Inhibition of mRNA levels by Oligonucleotides Against RPA1

Fig. 10



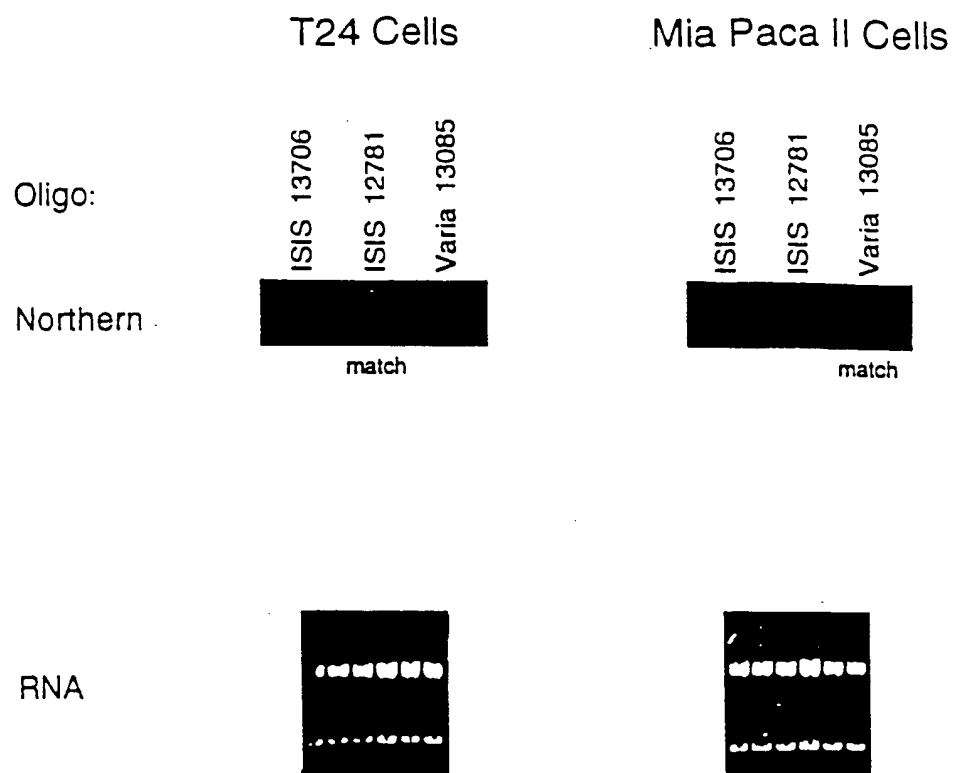
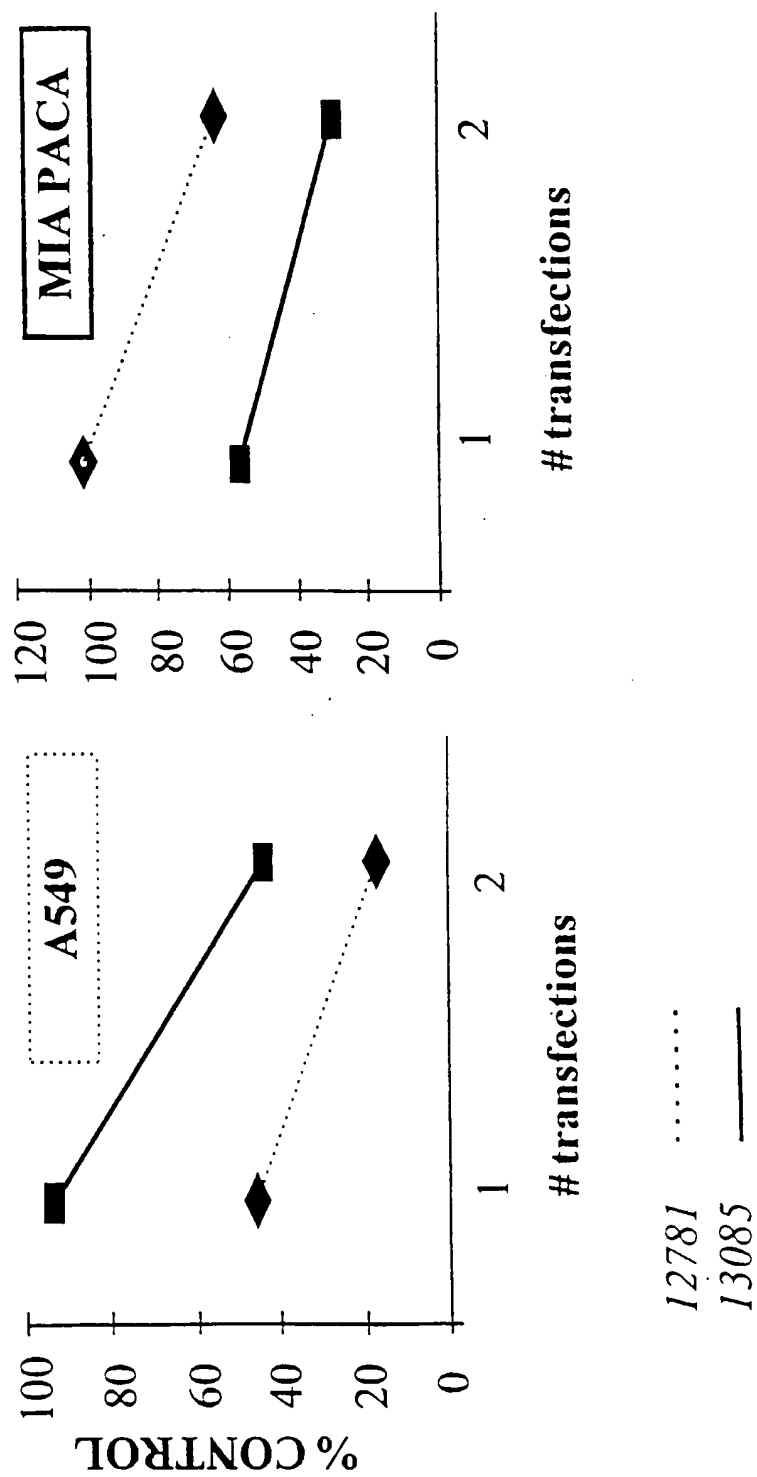


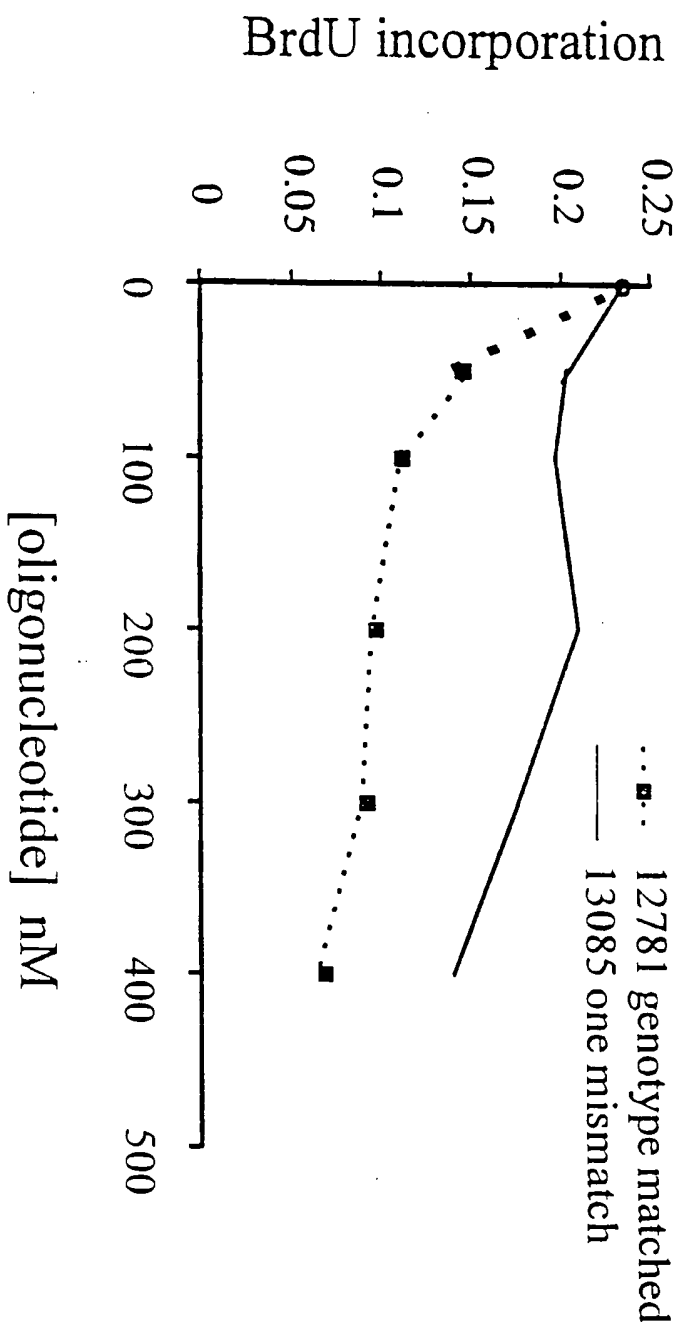
Fig. 11

Fig. 12



Variance Specific Inhibition of A549 Cell Proliferation by Oligonucleotides Against RPA1

Fig. 13



Variance Specific Cell Killing of A549 Cells by Oligonucleotides Against RPA1

Fig. 14

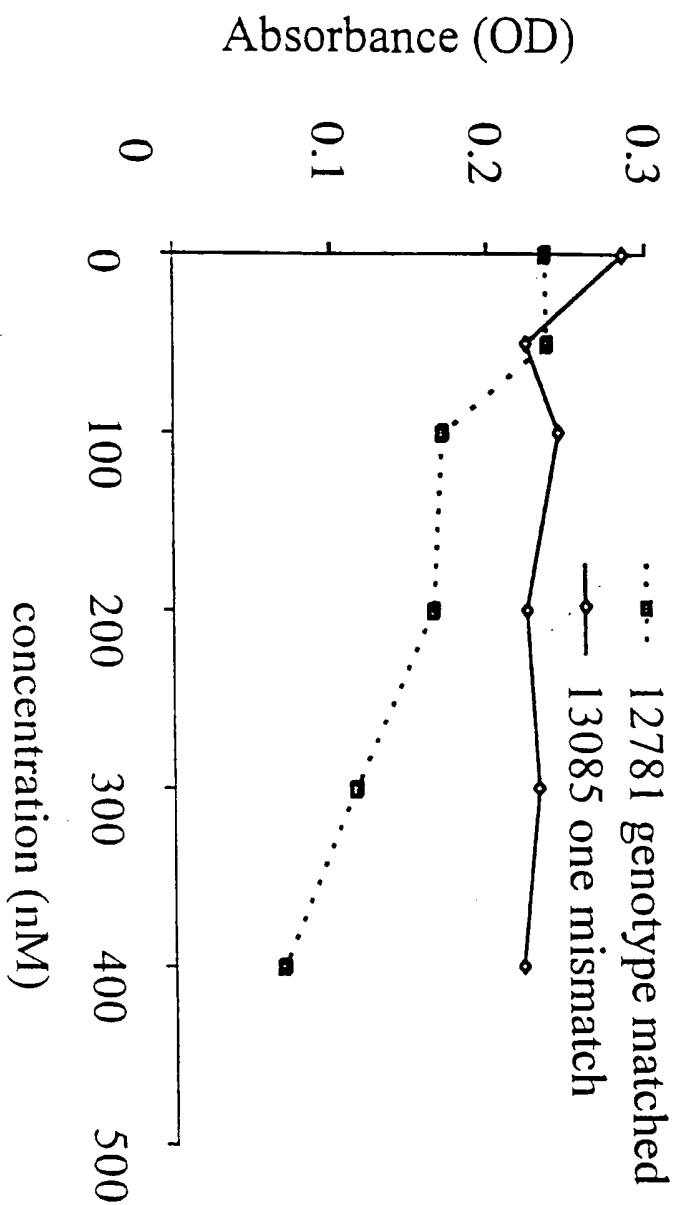
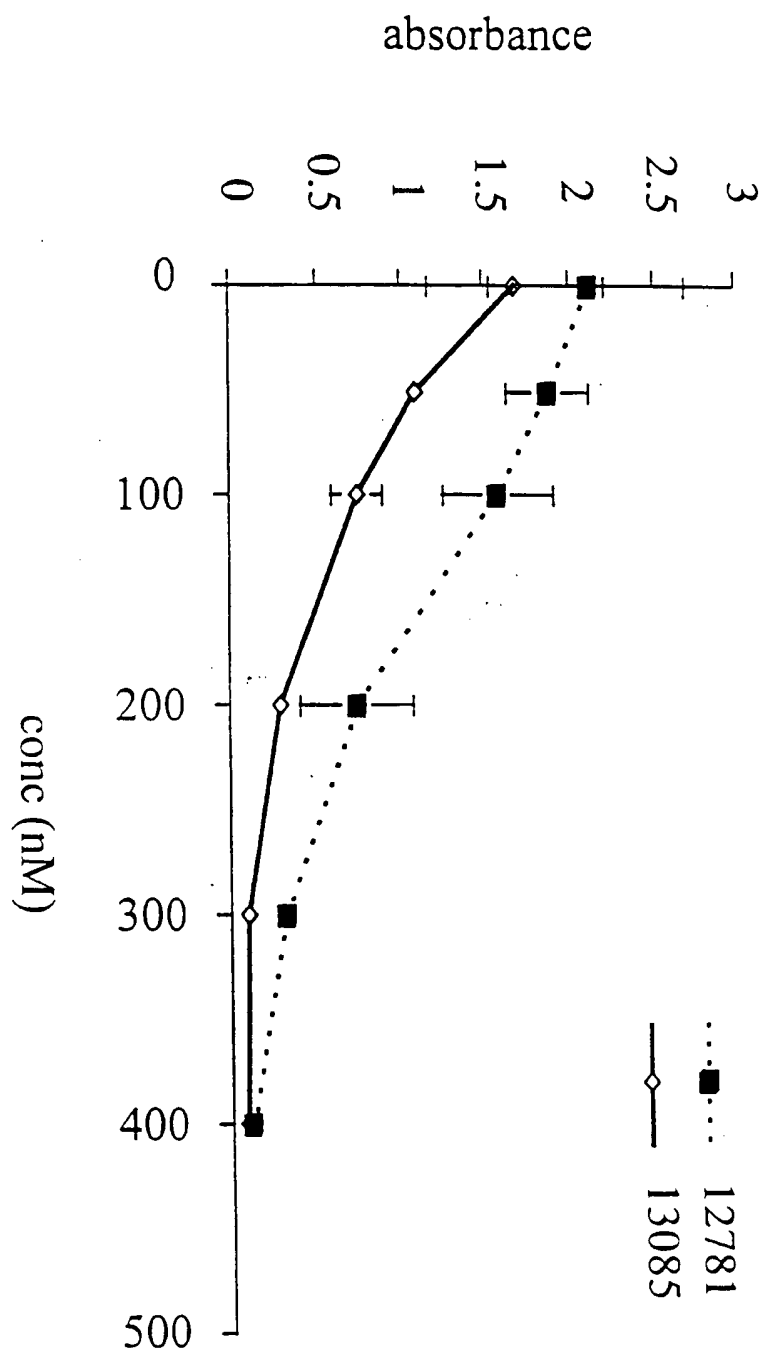


Fig. 15

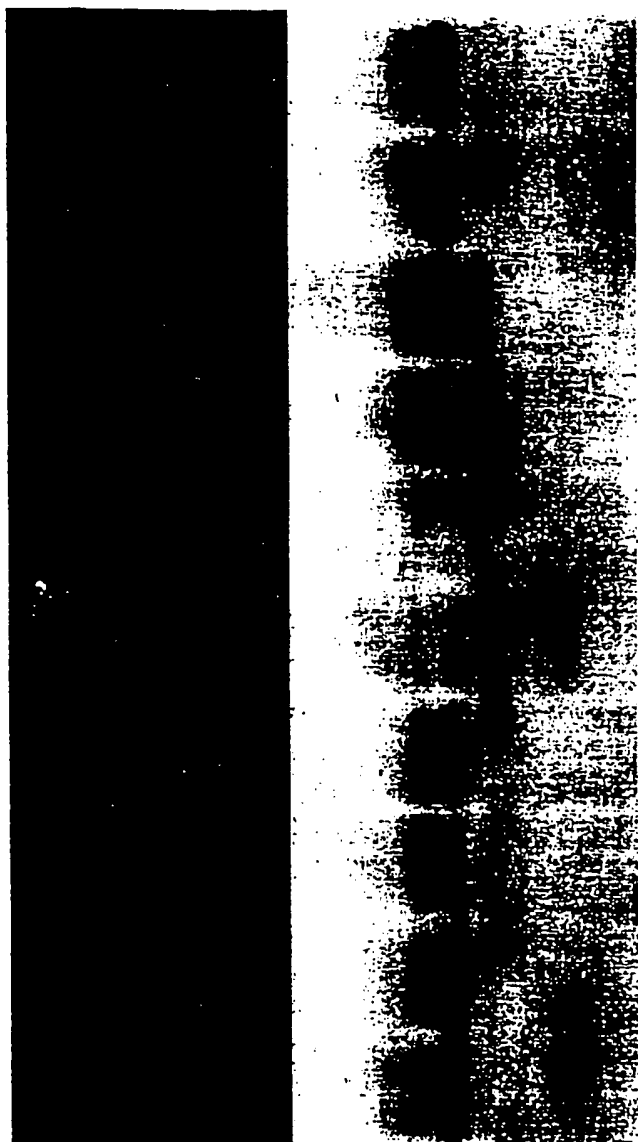


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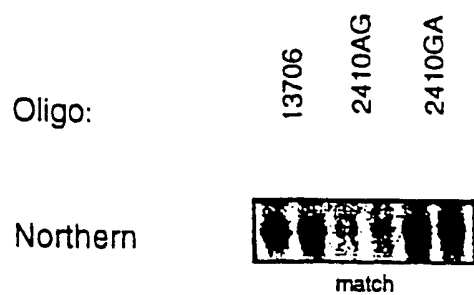
Suppression of Ribonucleotide Reductase mRNA

RR1030 RR1031 RR2410ga RR2410ag 13704

Fig. 16



MDA-MB 468 Cells



RNA

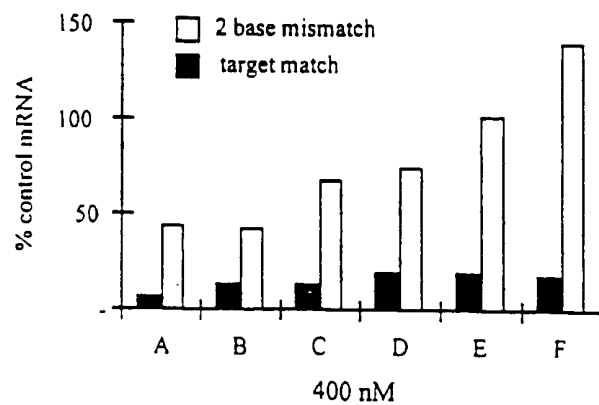


Fig. 17

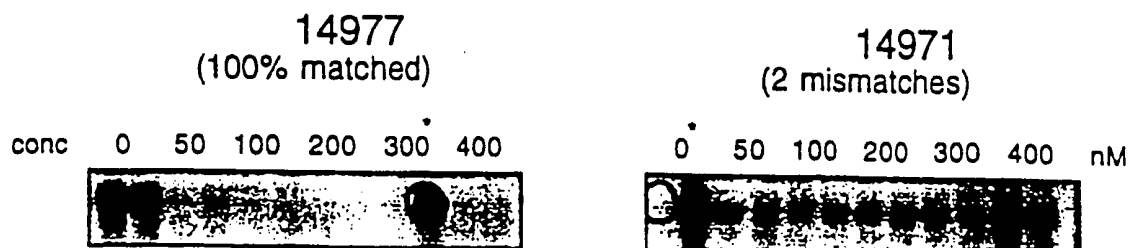
Fig. 18

Research Collaboration

	* *
A	ACAGCCACTTATGTCATGGT
B	ACAGCCACTTATGTCATGGT
C	<u>ACAGCCACTTATGTCATGGT</u>
D	CACTTATGTCATGGTATTCA
E	CACTTATGTCATGGTATTCA
F	<u>CACTTATGTCATGGTATTCA</u>

Improved Allele-Specificity with
Advanced Chemistry

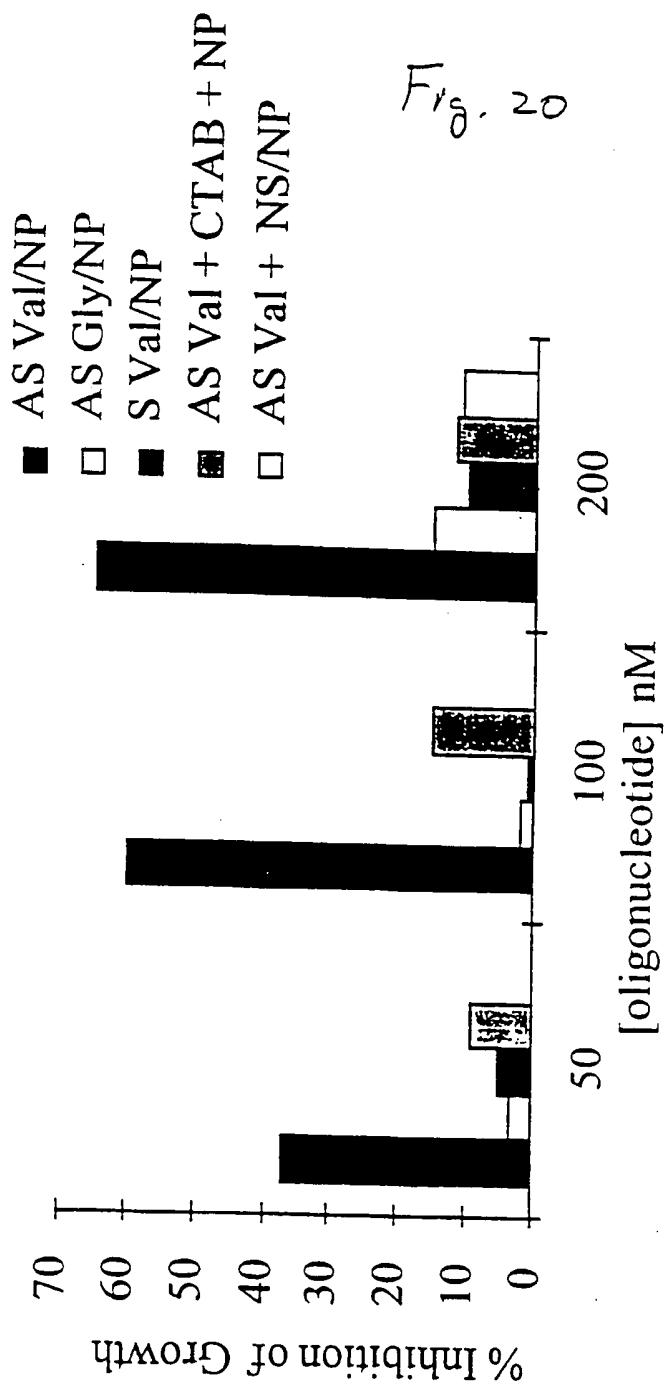
Effect of Antisense Oligomers on Glutamyl-
prolyl-tRNA Synthetase (EPRS) mRNA levels
(duplicates)



*circled samples were switched
when loaded on to the gel

Fig. 19

Example: Allele-Specific Inhibition of *Ras*



Schwab et al., 1994



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/00, C07K 14/00, A61K 35/00, C12N 15/00	A3	(11) International Publication Number: WO 98/41648 (43) International Publication Date: 24 September 1998 (24.09.98)
(21) International Application Number: PCT/US98/05419 (22) International Filing Date: 19 March 1998 (19.03.98) (30) Priority Data: 60/041,057 20 March 1997 (20.03.97) US (71) Applicant (for all designated States except US): VARIAGEN- ICS, INC. [US/US]; One Kendall Square, Building 400, Cambridge, MA 02139-1562 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): HOUSMAN, David [US/US]; 64 Homer Street, Newton, MA 02159 (US). LEDLEY, Fred, D. [US/US]; 433 Grove Street, Needham, MA 02192 (US). STANTON, Vincent, P., Jr. [US/US]; 32 Royal Road, Belmont, MA 02178 (US). (74) Agents: WARBURG, Richard, J. et al.; Lyon & Lyon LLP, Suite 4700, 633 West Fifth Street, Los Angeles, CA 90071-2066 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 29 April 1999 (29.04.99)
(54) Title: TARGET GENES FOR ALLELE-SPECIFIC DRUGS (57) Abstract <p>This disclosure concerns genetic targets which have been found to be useful for allele specific anti-tumor therapy. The strategy for such therapy involves the steps of: (1) identification of alternative alleles of genes coding for proteins essential for cell viability or cell growth and the loss of one of these alleles in cancer cells due to loss of heterozygosity (LOH) and (2) the development of inhibitors with high specificity for the single remaining alternative allele of the essential gene retained by the tumor cell after LOH. Particular categories of appropriate target genes are described, along with specific exemplary genes within those categories and methods of using such target genes.</p>		

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INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12Q1/00 C07K14/00 A61K35/00 C12N15/00		International Application No PCT/US 98/05419
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12Q		
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Electronic data base consulted during the international search (name of data base and, where practical, search terms used)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 03335 A (HOUSMAN DAVID E ;K O TECHNOLOGY INC (US)) 2 February 1995 cited in the application see the whole document ---	1,13,21, 29,37, 38,53, 54,69, 77-79, 101,109
A	WO 97 04087 A (KRUPP GUIDO ;MARGET MATTHIAS (DE); WESTPHAL ECKHARD (DE); MUELLER) 6 February 1997 ---	
A	WO 94 11494 A (UNIV JEFFERSON ;PROCKOP DARWIN (US); COLIGE ALAIN (BE); BASERGA RE) 26 May 1994 ---	
A	US 5 491 064 A (LICHY JACK H ET AL) 13 February 1996 ---	
-/-		
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex.		
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Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer <div style="text-align: center; font-weight: bold;">MOLINA GALAN E.</div>

INTERNATIONAL SEARCH REPORT

Intern. Application No

PCT/US 98/05419

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>WO 97 32024 A (TRINITY COLLEGE DUBLIN ;FARRAR GWENYTH JANE (IE); HUMPHRIES PETER) 4 September 1997</p> <p>see the whole document -----</p>	<p>1,13,21, 29,37, 38,53, 54,69, 77-79, 101,109</p>

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/05419

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 37, 53, 69 and 109 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1, 13, 21, 29, 37, 38, 53, 54, 69, 77-79, 101 and 109

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1, 13, 21, 29, 37, 38, 53, 54, 69, 77-79, 101 and 109

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required for cell proliferation wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

2. Claims: 2, 14, 22, 30, 39, 40, 55, 56, 70, 80-82, 102 and 110

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

3. Claims: 3, 15, 23, 31, 41, 42, 57, 58, 71, 83-85, 103 and 111

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain organic compounds at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

4. Claims: 4, 16, 24, 32, 43, 44, 59, 60, 72, 86-88, 104 and 112

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain cellular proteins at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

and pharmaceutical compositions comprising them.

5. Claims: 5, 17, 25, 33, 45, 46, 61, 62, 73, 89-91,
105 and 113

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain cellular nucleotides at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

6. Claims: 6, 18, 26, 34, 47, 48, 63, 64, 74, 92-94,
106 and 114

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain the integrity and function of cellular and subcellular structures wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

7. Claims: 7-10, 19, 27, 35, 49, 50, 65, 66, 75, 95-97 and 107

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and being located on a high frequency loss of heterozygosity chromosomal arm region, wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

8. Claims: 11, 12, 20, 28, 36, 51, 52, 67, 68, 76,
98-100 and 108

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability having at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for that gene and wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

such inhibitors and pharmaceutical compositions comprising them.

9. Claims: 115-129

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene conditionally vital for cell growth or viability wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

10. Claims: 131-146

Methods using inhibitors targeting at least one but less than all alleles of a gene vital for cell growth or viability wherein cells not targeted by the inhibitor have at least one alternative variant allele related to transplantation and engraftment.

11. Claims: 147-150

Methods for separating a cell from a mixture using allele specific binding compounds targeting at least one but less than all alleles of a gene wherein cells not targeted by the compound have at least one alternative variant allele.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/05419

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9503335 A	02-02-1995	AU 690131 B	23-04-1998
		AU 7405994 A	20-02-1995
		CA 2168096 A	02-02-1995
		EP 0714410 A	05-06-1996
		JP 9500650 T	21-01-1997
		US 5702890 A	30-12-1997
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